

GenCore version 5.1.1.8  
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OM protein - protein search, using sw model

Run on: May 8, 2006, 21:08:16 ; Search time 169 Seconds  
(without alignments) 205.206 Million cell

**Title:** US-10-716-824-2

Perfect score: 444

Sequence: 1 MKGWGLALLGALLGTAWA.....QSVVEVTVTPPNKVAHSGF 83

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

## Listing first 45 summaries

Database :

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Database : Published Applications_AA_Main:*
1: /csm2_6/prodata/1/pubapp/us07_PUBCOMB.pep.*
2: /csm2_6/prodata/1/pubapp/us08_PUBCOMB.pep.*
3: /csm2_6/prodata/1/pubapp/us09_PUBCOMB.pep.*
4: /csm2_6/prodata/1/pubapp/us10A_PUBCOMB.pep.*
5: /csm2_6/prodata/1/pubapp/us10B_PUBCOMB.pep.*
6: /csm2_6/prodata/1/pubapp/us11_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
1	444	100.0	83	4	US-10-082-502-2	Sequence 2, Appli	
2	444	100.0	83	4	US-10-716-824-2	Sequence 2, Appli	
3	444	100.0	83	5	US-10-932-376-2	Sequence 2, Appli	
4	444	100.0	84	3	US-09-978-360A-716	Sequence 716, App	
5	444	100.0	84	4	US-10-319-763-204	Sequence 204, App	
6	444	100.0	84	4	US-10-632-983-63	Sequence 63, Appl	
7	410.5	92.5	97	4	US-10-319-763-110	Sequence 110, App	
8	369	83.1	182	3	US-09-978-360A-717	Sequence 717, App	
9	369	83.1	182	4	US-10-028-072-174	Sequence 174, App	
10	369	83.1	182	4	US-10-140-808-174	Sequence 174, App	
11	369	83.1	182	4	US-10-121-049-174	Sequence 174, App	
12	369	83.1	182	4	US-10-123-904-174	Sequence 174, App	
13	369	83.1	182	4	US-10-140-470-174	Sequence 174, App	
14	369	83.1	182	4	US-10-175-746-174	Sequence 174, App	
15	369	83.1	182	4	US-10-176-918-174	Sequence 174, App	
16	369	83.1	182	4	US-10-176-921-174	Sequence 174, App	
17	369	83.1	182	4	US-10-137-865-174	Sequence 174, App	
18	369	83.1	182	4	US-10-140-474-174	Sequence 174, App	
19	369	83.1	182	4	US-10-142-431-174	Sequence 174, App	
20	369	83.1	182	4	US-10-143-114-174	Sequence 174, App	
21	369	83.1	182	4	US-10-142-419-174	Sequence 174, App	
22	369	83.1	182	4	US-10-123-262-174	Sequence 174, App	
23	369	83.1	182	4	US-10-142-423-174	Sequence 174, App	
24	369	83.1	182	4	US-10-121-050-174	Sequence 174, App	
25	369	83.1	182	4	US-10-141-755-174	Sequence 174, App	
26	369	83.1	182	4	US-10-143-032-174	Sequence 174, App	
27	369	83.1	182	4	US-10-123-108-174	Sequence 174, App	

## ALIGNMENTS

## RESULT 1

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US-10-082-502-2
; Sequence 2, Application US/10082502
; Publication No. US20030171542A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Jelinek, Laura J.
; TITLE OF INVENTION: Mammalian Secretory Protein
; FILE REFERENCE: 97-11C2
; CURRENT APPLICATION NUMBER: US/10/082,502
; CURRENT FILING DATE: 2001-10-19
; PRIORITY APPLICATION NUMBER: 09/318,028
; PRIORITY FILING DATE: 1999-05-25
; PRIORITY APPLICATION NUMBER: 09/109,808
; PRIORITY FILING DATE: 1998-07-02
; PRIORITY APPLICATION NUMBER: 60/089,899
; PRIORITY FILING DATE: 1998-06-17
; PRIORITY APPLICATION NUMBER: 60/085,983
; PRIORITY FILING DATE: 1998-05-19
; PRIORITY APPLICATION NUMBER: 60/051,704
; PRIORITY FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-082-502-2

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Qy	1	MKGWGWLALLGALLGTANARRSQDLHGCACRALVDELEWEIAQVDPKTIQMGSFRINP	60	
Dd	1	MKGWGWLALLGALLGTANARRSQDLHGCACRALVDELEWEIAQVDPKTIQMGSFRINP	60	
Qy	61	DGQSQSVVEVTIVPPNKNVAHSGF	83	
Dd	61	DGQSQSVVEVTIVPPNKNVAHSGF	83	

RESULT 2  
US-10-716-824-2  
; Sequence 2, Application US/10716824  
; Publication No. US20040110927A1  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Jelinek, Laura J.  
; TITLE OF INVENTION: Mammalian Secretory protein - 9

FILE REFERENCE: 97-11C2  
CURRENT APPLICATION NUMBER: US/10/716,824  
CURRENT FILING DATE: 2003-11-19  
PRIOR FILING DATE: 2003-11-19  
PRIOR FILING DATE: 2001-10-19  
PRIOR FILING DATE: 2001-10-19  
PRIOR FILING DATE: 1999-05-25  
PRIOR FILING DATE: 1999-05-25  
PRIOR FILING DATE: 1998-07-02  
PRIOR FILING DATE: 1998-07-02  
PRIOR FILING DATE: 1998-06-17  
PRIOR FILING DATE: 1998-06-17  
PRIOR FILING DATE: 1998-05-19  
PRIOR FILING DATE: 1998-05-19  
PRIOR FILING DATE: 1997-07-03  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 83  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-716-824-2

Query Match 100.0%; Score 444; DB 4; Length 83;  
Best Local Similarity 100.0%; Pred. No. 1.1e-44;  
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSPRNP 60  
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Db 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSPRNP 60  
|||||

Qy 61 DGSQSVVEVTVPNNKVAHSGF 83  
|||||

Db 61 DGSQSVVEVTVPNNKVAHSGF 83  
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## RESULT 3

US-10-932-376-2  
Sequence 2, Application US/10932376  
Publication No. US20050124801A1  
GENERAL INFORMATION:  
APPLICANT: Sheppard, Paul O.  
APPLICANT: Jelinek, Laura J.  
TITLE OF INVENTION: Mammalian Secretory Protein - 9  
FILE REFERENCE: 97-11C2  
CURRENT APPLICATION NUMBER: US/10/932,376  
CURRENT FILING DATE: 2004-09-02  
PRIOR FILING DATE: 2001-10-19  
PRIOR FILING DATE: 2001-10-19  
PRIOR FILING DATE: 1999-05-25  
PRIOR FILING DATE: 1999-05-25  
PRIOR FILING DATE: 1998-07-02  
PRIOR FILING DATE: 1998-07-02  
PRIOR FILING DATE: 1998-06-17  
PRIOR FILING DATE: 1998-06-17  
PRIOR FILING DATE: 1998-05-19  
PRIOR FILING DATE: 1998-05-19  
PRIOR FILING DATE: 1997-07-03  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 83  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-932-376-2

Query Match 100.0%; Score 444; DB 5; Length 83;  
Best Local Similarity 100.0%; Pred. No. 1.1e-44;  
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSPRNP 60  
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Db 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSPRNP 60  
Qy 61 DGSQSVVEVTVPNNKVAHSGF 83  
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Db 61 DGSQSVVEVTVPNNKVAHSGF 83  
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## RESULT 4

US-09-978-360A-716  
Sequence 716, Application US/09978360A  
Publication No. US20040110939A1  
GENERAL INFORMATION:  
APPLICANT: Edwards, Jean-Baptiste Dumas Milne  
APPLICANT: Duclert, Aymeric  
APPLICANT: Bougueleret, Lydie  
APPLICANT: Jobert, Severin  
APPLICANT: Ciusel, Catherine  
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides  
FILE REFERENCE: 56.US4.CIP  
CURRENT APPLICATION NUMBER: US/09/978,360A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: US 60/066,677  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: US 60/069,957  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: US 60/074,121  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: US 60/081,563  
PRIOR FILING DATE: 1998-04-13  
PRIOR APPLICATION NUMBER: US 60/096,116  
PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: US 60/099,273  
PRIOR FILING DATE: -09-04  
PRIOR APPLICATION NUMBER: US 09/191,997  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: US 09/215,435  
PRIOR FILING DATE: 1998-12-17  
PRIOR APPLICATION NUMBER: PCT/IB98/02122  
PRIOR FILING DATE: 1998-12-17  
PRIOR APPLICATION NUMBER: US 09/247,155  
PRIOR FILING DATE: 1999-02-09  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 810  
SOFTWARE: Patent.pm  
SEQ ID NO 716  
LENGTH: 84  
TYPE: PRT  
ORGANISM: Homo sapiens  
NAME/KEY: SIGNAL  
LOCATION: -20...-1  
US-09-978-360A-716

Query Match 100.0%; Score 444; DB 3; Length 84;  
Best Local Similarity 100.0%; Pred. No. 1.1e-44;  
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSPRNP 60  
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Db 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSPRNP 60  
|||||

Qy 61 DGSQSVVEVTVPNNKVAHSGF 83  
|||||

Db 61 DGSQSVVEVTVPNNKVAHSGF 83  
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## RESULT 5

US-10-319-763-204  
Sequence 204, Application US/10319763  
Publication No. US2003014490A1  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
APPLICANT: Duclert, Aymeric



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; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56.US4.CIP
; CURRENT APPLICATION NUMBER: US/09/978.360A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435
; PRIOR FILING DATE: 1998-12-17
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; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent.pm
; SEQ ID NO 717
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -20...-1
US-09-978-360A-717

Query Match      83.1%; Score 369; DB 3; Length 182;
Best Local Similarity 100.0%; Pred. No. 2.2e-35;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWEIAQVDPKKTIQMSFRINP 60
Db 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWEIAQVDPKKTIQMSFRINP 60

Qy 61 DGSQSVVEV 69
Db 61 DGSQSVVEV 69

RESULT 9
US-10-028-072-174
; Sequence 174, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Degnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang

; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
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; PRIOR FILING DATE: 1997-11-17
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; PRIOR APPLICATION NUMBER: 60/088026  
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; PRIOR APPLICATION NUMBER: 60/088730  
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; PRIOR FILING DATE: 1998-06-10  
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; PRIOR APPLICATION NUMBER: 60/091360  
; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091519  
; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07

Query Match 83.1%; Score 369; DB 4; Length 182;

Best Local Similarity 100.0%; Pred. No. 2.2e-35;

Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDSLEWIEIAQVDPKKTQMGSFRINP 60  
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Db 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDSLEWIEIAQVDPKKTQMGSFRINP 60  
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Qy 61 DGSQSVVEV 69  
|||||

Db 61 DGSQSVVEV 69  
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RESULT 10

US-10-140-808-174

; Sequence 174, Application US/10140808

; Publication No. US20030017563A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C182

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; CURRENT APPLICATION NUMBER: US/10/140,808
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 174
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-808-174

Query Match      83.1%; Score 369; DB 4; Length 182;
Best Local Similarity 100.0%; Pred. No. 2.2e-35;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWEIAQVDPKKTQMGSPRNP 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWEIAQVDPKKTQMGSPRNP 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 61 DGSQSVVEV 69
   |||||||||||
Db 61 DGSQSVVEV 69

RESULT 11
US-10-121-049-174
; Sequence 174, Application US/10121049
; Publication No. US20030022239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 174
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-904-174

Query Match      83.1%; Score 369; DB 4; Length 182;
Best Local Similarity 100.0%; Pred. No. 2.2e-35;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWEIAQVDPKKTQMGSPRNP 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWEIAQVDPKKTQMGSPRNP 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 61 DGSQSVVEV 69
   |||||||||||
Db 61 DGSQSVVEV 69

RESULT 12
US-10-123-904-174
; Sequence 174, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C160
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
```

; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 174

; LENGTH: 182

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-140-470-174

Query Match 83.1%; Score 369; DB 4; Length 182;

Best Local Similarity 100.0%; Pred. No. 2.2e-35;

Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWEIAQVDPKKTQMGSRINP 60

Db 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWEIAQVDPKKTQMGSRINP 60

Qy 61 DGSQSVVEV 69

Db 61 DGSQSVVEV 69

RESULT 14

US-10-175-746-174

; Sequence 174, Application US/10175746

; Publication No. US20030027270A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Deanoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P330R1C353

; CURRENT APPLICATION NUMBER: US/10/175,746

; CURRENT FILING DATE: 2002-06-19

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 174

; LENGTH: 182

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-175-746-174

Query Match 83.1%; Score 369; DB 4; Length 182;

Best Local Similarity 100.0%; Pred. No. 2.2e-35;

Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWEIAQVDPKKTQMGSRINP 60

Db 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWEIAQVDPKKTQMGSRINP 60

Qy 61 DGSQSVVEV 69

Db 61 DGSQSVVEV 69

RESULT 15

US-10-176-918-174

; Sequence 174, Application US/10176918

; Publication No. US20030027275A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Deanoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P330R1C382

; CURRENT APPLICATION NUMBER: US/10/176,918

; CURRENT FILING DATE: 2002-06-20

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 174

; LENGTH: 182

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-176-918-174

Query Match 83.1%; Score 369; DB 4; Length 182;

Best Local Similarity 100.0%; Pred. No. 2.2e-35;

Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWEIAQVDPKKTQMGSRINP 60

Db 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWEIAQVDPKKTQMGSRINP 60

Qy 61 DGSQSVVEV 69

Db 61 DGSQSVVEV 69

Search completed: May 8, 2006, 21:12:01

Job time : 170 secs

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 8, 2006, 20:49:24 ; Search time 186 Seconds  
(without alignments)  
196.067 Million cell updates/sec

Title: US-10-716-824-2  
Perfect score: 444  
Sequence: 1 MKGKGLALLGALLGTAWA.....QSVVEVTVPKVAHSGF 83

Scoring table:  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003s.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	444	100.0	83	3 AAY15130	Aay15130 Human Zsi
2	444	100.0	84	2 AAW88469	Aaw88469 Human sec
3	444	100.0	84	2 AAY36199	Aay36199 Human sec
4	444	100.0	84	6 ADA57311	Ada57311 Human sec
5	444	100.0	84	7 ADC74386	Adc74386 Human sec
6	444	100.0	84	7 ADD38010	Add38010 Human sec
7	444	100.0	84	7 ADJ46051	Adj46051 Novel hum
8	444	100.0	84	8 ADP19460	Adp19460 Human sec
9	444	100.0	85	2 AAY30716	Aay30716 Amino aci
10	410.5	92.5	97	2 AAY36152	Aay36152 Human sec
11	410.5	92.5	97	7 ADJ45957	Adj45957 Novel hum
12	369	83.1	168	8 ADP29267	Adp29267 Human sec
13	369	83.1	182	2 AAW88474	Aaw88474 Human sec
14	369	83.1	182	2 AAY36200	Aay36200 Human sec
15	369	83.1	182	3 AAY15135	Aay15135 Human Zsi
16	369	83.1	182	3 AAY52391	Aay52391 Human tra
17	369	83.1	182	4 AAU12258	Aau12258 Human PRO
18	369	83.1	182	5 AAB97063	Aab97063 Transmem
19	369	83.1	182	5 ABB09717	Abb09717 Amino aci
20	369	83.1	182	6 ABO17702	Abo17702 Novel hum
21	369	83.1	182	6 ADA56723	Ada56723 Human sec
22	369	83.1	182	6 ABU80956	Abu80956 Human PRO
23	369	83.1	182	6 ABU66656	Abu66656 Human PRO
24	369	83.1	182	6 ABU59737	Abu59737 Novel sec

25	369	83.1	182	6 ABO24927	AbO24927 Human sec
26	369	83.1	182	6 ABU66932	Abu66932 Human sec
27	369	83.1	182	6 ADA45693	Ada45693 Novel hum
28	369	83.1	182	6 ADA76124	Ada76124 Human PRO
29	369	83.1	182	6 ADA18774	Ada18774 Human PRO
30	369	83.1	182	6 ADA61397	Ada61397 Homo sapi
31	369	83.1	182	6 ADB19182	AdB19182 Novel hum
32	369	83.1	182	6 ADB27723	AdB27723 Human PRO
33	369	83.1	182	6 ADA86202	Ada86202 Novel hum
34	369	83.1	182	6 ADB15766	AdB15766 Human PRO
35	369	83.1	182	6 ADA47552	Ada47552 Human PRO
36	369	83.1	182	6 ADA67347	Ada67347 Human PRO
37	369	83.1	182	6 ADB30354	AdB30354 Human PRO
38	369	83.1	182	6 ADA85650	Ada85650 Novel hum
39	369	83.1	182	6 ADA96862	Ada96862 Human PRO
40	369	83.1	182	6 ADA79166	Ada79166 Human PRO
41	369	83.1	182	6 ADA87305	Ada87305 Novel hum
42	369	83.1	182	6 ADB16507	AdB16507 Human PRO
43	369	83.1	182	6 ADA91599	Ada91599 Novel hum
44	369	83.1	182	6 ADB14662	AdB14662 Human PRO
45	369	83.1	182	6 ADB18623	AdB18623 Novel hum

ALIGNMENTS

RESULT 1  
AAY15130  
ID AAY15130 standard; protein; 83 AA.  
XX  
AC AAY15130;  
XX  
DT 07-FEB-2000 (first entry)  
XX  
DE Human Zsig9 secretory protein partial sequence.  
XX  
KW Secretory protein-9; Human Zsig9; chromosome 12q15 region; tumour;  
KW overexpression; antagonist; antibody; antisease nucleotide; detection;  
KW treatment; receptor; radio-label; fusion; polypeptide toxin; technique;  
KW down-regulation; probe; diagnostic; therapeutic; cancer; brain; liver;  
KW stomach; lymphoma.  
XX  
OS Homo sapiens.  
XX  
Key Location/Qualifiers  
FH Peptide 1..20  
FT /label= Signal\_sequencá  
FT Protein 21..83  
FT /label= Mature\_Zsig9\_secretory\_protein  
FT /note= "The sequence according to the specification has  
84 amino acids, but only 83 amino acids are shown in the  
sequence listing"  
WO9960405-A1.  
25-NOV-1999.  
19-MAY-1999; 99WO-US011107.  
19-MAY-1998; 98US-00081183.  
(ZYMO ) ZYMOGENETICS INC.  
Moore EE, Taft DW;  
WPI; 2000-039447/03.  
N-PSDE; AAZ08284.  
Detecting tumors using antibodies, antagonists and antisense nucleotides  
to secretory protein-9 (Zsig9).  
Claim 1; Page 30; 45pp; English.  
XX

CC The present protein sequence is the secretory protein-9, Zsig9. This  
 CC sequence is mapped to the human chromosome 12q15 region. It is  
 CC overexpressed in tumours. Antagonists, antibodies and antisense  
 CC nucleotides to Zsig9 are useful for detecting and treating tumours. The  
 CC antagonist may be an antibody or receptor to Zsig9 and it may be radio-  
 CC labelled or fused to a polypeptide toxin. It can be used for down-  
 CC regulating the overexpression of Zsig9. The gene sequence can be used as  
 CC nucleic acid probes to detect RNA encoding Zsig9. The Zsig9 sequence  
 CC facilitates improved diagnostic and therapeutic techniques for detecting  
 CC and treating cancers, especially of the brain, liver, stomach, lymphoma  
 CC etc., at an early stage  
 XX  
 SQ Sequence 83 AA;

Query Match 100.0%; Score 444; DB 3; Length 83;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-47;  
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGWMLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTIQMGSPRNP 60  
 Db 1 MKGWMLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTIQMGSPRNP 60

Qy 61 DGSQSVVEVTVPNNKVAHSGF 83

Db 61 DGSQSVVEVTVPNNKVAHSGF 83

## RESULT 2

AAW88469  
 ID AAW88469 standard; protein; 84 AA.

XX AAW88469;

DT 10-MAY-1999 (first entry)

XX Human secretory peptide-9 (Zsig9).

XX Secretory peptide-9; Zsig9; human; tumour marker; cancer; therapy;  
 XX diagnosis; growth enhancer.

OS Homo sapiens.

XX Key Location/Qualifiers  
 FH Peptide 1..20

FT Protein /note= "signal peptide"

FT Protein 21..84

FT Disulfide-bond 28..31

XX WO9901554-A1,

XX 14-JAN-1999.

XX 02-JUL-1998; 98WO-US013859.

XX 03-JUL-1997; 97US-0051704P.

XX 03-JUL-1997; 97US-0088088.

XX 19-MAY-1998; 98US-00081338.

XX 19-MAY-1998; 98US-0085983P.

XX 17-JUN-1998; 98US-00099005.

XX 17-JUN-1998; 98US-0089899P.

XX (ZYMO ) ZYMOGENETICS INC.

XX Sheppard PO, Jelinek LJ, Jaspers SR, Whitmore TE;

XX WPI; 1999-106055/09.

XX N-PSDB; AAX06968.

XX New mammalian secretory peptide-9 (Zsig9) - used as a growth enhancer for  
 XX placenta, liver and heart, and as an indicator of cancer.

PS Claim 8; Page 67; 85pp; English.

XX

CC This is the amino acid sequence of novel human secretory peptide-9, or  
 CC Zsig9, a polypeptide that is overexpressed in a number of human tumours  
 CC including brain, liver, lung, oesophageal, stomach, colon, rectal,  
 CC thyroid and lymphoma tumors. Thus, Zsig can be used as an indicator for  
 CC cancer. Zsig9 cDNA (see AAX06968) was discovered in a placenta clone from  
 CC a full-term pregnancy cDNA library. The invention provides Zsig9  
 CC polypeptides (see AAW88469-77) including mature polypeptides, other  
 CC processed forms, variants and mouse orthologues, and polynucleotides (see  
 CC AAX06968-70) encoding them. Antibodies raised against Zsig9 can be used  
 CC as diagnostic agents to determine the presence of Zsig9, and thus the  
 CC presence of cancer. They can also be labelled with radioisotopes or fused  
 CC with toxins and used to treat tumours which overexpress Zsig9. Antisense  
 CC nucleotides derived from Zsig9 cDNA can also be used to inhibit the  
 CC growth of tumour cells. Zsig9 proteins can be used to enhance the growth  
 CC or development of the placenta, heart or liver  
 XX  
 SQ Sequence 84 AA;

Query Match 100.0%; Score 444; DB 2; Length 84;

Best Local Similarity 100.0%; Pred. No. 4.4e-47;

Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGWMLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTIQMGSPRNP 60

Db 1 MKGWMLALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTIQMGSPRNP 60

Qy 61 DGSQSVVEVTVPNNKVAHSGF 83

Db 61 DGSQSVVEVTVPNNKVAHSGF 83

## RESULT 3

AAAY36199

ID AAY36199 standard; protein; 84 AA.

XX AAY36199;

DT 23-SEP-1999 (first entry)

XX Human secreted protein #71.

XX Secreted protein; human; cytostatic; thrombotic; osteopathic; forensic;  
 XX diagnostic; gene therapy; chromosome mapping; secretion vector.

OS Homo sapiens.

XX WO9925825-A2.

XX 27-MAY-1999.

XX 13-NOV-1998; 98WO-IB001862.

XX 13-NOV-1997; 97US-0066677P.

XX 17-DEC-1997; 97US-0069957P.

XX 09-FEB-1998; 98US-0074121P.

XX 13-APR-1998; 98US-0081563P.

XX 10-AUG-1998; 98US-0096116P.

XX 04-SEP-1998; 98US-0099273P.

XX (GEST ) GENSET.

XX Bougueleret L, Duclert A, Dumas Milne Edwards J;

XX WPI; 1999-347472/29.

XX N-PSDB; AAX97883.

XX Extended cDNAs encoding secreted proteins.

PS Claim 7; Page 298-299; 307pp; English.

XX AAY36129-Y36222 represent novel human secreted proteins encoded by the  
 CC extended cDNA sequences represented in AAX97813-X97906. The proteins of

CC the invention have cytostatic, thrombotic and osteopathic activity. The  
 CC extended cDNAs can be used to express secreted proteins or parts of them  
 CC or to obtain antibodies capable of binding to the secreted proteins. They  
 CC may also be used in diagnostic, forensic, gene therapy and chromosome  
 CC mapping procedures. Uses also include design of expression vectors and  
 CC secretion vectors  
 XX  
 SQ Sequence 84 AA;

Query Match 100.0%; Score 444; DB 2; Length 84;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-47;  
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWIAQVDPKKTQMGSFRINP 60  
 Db 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWIAQVDPKKTQMGSFRINP 60  
 Qy 61 DGSQSVVEVTVPNNKVAHSGF 83  
 Db 61 DGSQSVVEVTVPNNKVAHSGF 83

RESULT 4  
 ADA57311 standard; protein; 84 AA.  
 XX  
 AC ADA57311;

XX 20-NOV-2003 (first entry)

XX Human secreted protein #5.

XX immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;  
 KW cytosstatic; cerebroprotective; neuroprotective; nootropic;  
 KW cardiovascular; antiarteriosclerotic; gene therapy;  
 KW human secreted protein; immune disorder; inflammation;  
 KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;  
 KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;  
 KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;  
 KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;  
 KW triple helix formation; antisense gene therapy; forensic biology.  
 XX

OS Homo sapiens.

XX WO2002102994-A2.

XX 27-DEC-2002.

XX 19-MAR-2002; 2002WO-US008278.

XX 21-MAR-2001; 2001US-0277340P.

XX 19-JUL-2001; 2001US-0306171P.

XX 13-NOV-2001; 2001US-0331287P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2003-167512/16.

XX N-FSDB; ADA56415.

XX New human secreted polypeptides and polynucleotides, useful for  
 PT diagnosing, treating or preventing e.g. immune disorders, inflammatory  
 PT conditions, respiratory disorders, cancers, CNS disorders, or  
 PT neurodegenerative disorders.  
 XX

XX Claim 13; SEQ ID NO 1501; 1754pp; English.

XX The invention relates to 592 new human secreted polypeptides useful for  
 CC diagnosing, treating or preventing e.g. immune disorders, inflammatory  
 CC conditions, respiratory disorders, cancers, CNS disorders, or  
 CC neurodegenerative disorders, or polypeptides comprising an amino acid  
 CC sequence at least 95% identical to the new sequences. The polypeptides,

CC antibodies or antibody fragments that bind to the polypeptides, nucleic  
 CC acids encoding the polypeptides, agonists or antagonists that binds to  
 CC the polypeptide, are useful in preparing diagnostic or pharmaceutical  
 CC compositions for diagnosing, treating or preventing an e.g. immune  
 CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,  
 CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and  
 CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders  
 CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative  
 CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and  
 CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The  
 CC polynucleotides are useful for chromosome identification, chromosome  
 CC mapping, for controlling gene expression through triple helix formation  
 CC or antisense DNA or RNA, in gene therapy, for identifying individuals  
 CC from minute biological samples, in forensic biology, and as hybridization  
 CC probes. The polypeptides are useful for as molecular weight markers on  
 CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)  
 CC gels, to raise antibodies, for testing biological activities, and for  
 CC treating or preventing neural disorders, immune system disorders,  
 CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,  
 CC renal, proliferative and/or cancerous diseases. This sequence corresponds  
 CC to one of the polypeptide of the invention. Note: The sequence data for  
 CC this patent did form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 84 AA;

Query Match 100.0%; Score 444; DB 6; Length 84;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-47;  
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWIAQVDPKKTQMGSFRINP 60  
 Db 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWIAQVDPKKTQMGSFRINP 60

Qy 61 DGSQSVVEVTVPNNKVAHSGF 83

Db 61 DGSQSVVEVTVPNNKVAHSGF 83

RESULT 5

ADC74386

ID ADC74386 standard; protein; 84 AA.

XX AC ADC74386;

XX 01-JAN-2004 (first entry)

XX Human secreted protein - SEQ ID 1019.

XX antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;  
 KW antidiabetic; immunosuppressive; dermatologic; nephrotropic;  
 KW antiparkinsonian; neuroprotective; nootropic; antibacterial; virucide;  
 KW fungicide; antiparasitic; antiarteriosclerotic; vulnerary; cytostatic;  
 KW haemopoietic; haematologic; anaemia; autoimmune disorder;  
 KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;  
 KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;  
 KW Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;  
 KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;  
 KW human.  
 XX

OS Homo sapiens.

XX WO2003038063-A2.

XX 08-MAY-2003.

XX 19-MAR-2002; 2002WO-US008277.

XX 21-MAR-2001; 2001US-0277340P.

XX 19-JUL-2001; 2001US-0306171P.

XX 13-NOV-2001; 2001US-0331287P.

```

PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Ruben SM;
XX WPI; 2003-430516/40.
XX DR N-PSDB; ADC73771.
XX PT New human secreted polypeptide for diagnosing, preventing or treating
XX PT hematopoietic or hematologic disorders (e.g. anemia), autoimmune
XX PT disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or
XX PT atherosclerosis).
XX PS Claim 16; SEQ ID NO 1019; 2272pp; English.
XX CC The invention relates to a novel human secreted polypeptide comprising a
XX CC defined sequence given in the specification. The polypeptide, nucleic
XX CC acid molecule, antibody, agonist or antagonist of the invention may be
XX CC useful for preparing a composition for diagnosing or treating a
XX CC haematopoietic or haematologic disorder such as anaemia, autoimmune
XX CC disorders such as rheumatoid arthritis, inflammation, Grave's disease,
XX CC diabetes, systemic lupus erythematosus or glomerulonephritis,
XX CC neurodegenerative disorders including Parkinson's disease and Alzheimer's
XX CC disease, wounds and hyperproliferative disorders including
XX CC atherosclerosis or cancer, as well as bacterial, viral, fungal or
XX CC parasitic infections. The polypeptide may also be used during gene
XX CC therapy procedures and for identifying a binding partner by contacting
XX CC the polypeptide with a binding partner and determining whether the
XX CC binding partner increases or decreases the activity of the polypeptide.
XX CC The current sequence is that of the human secreted protein of the
XX CC invention.
XX SQ Sequence 84 AA;

Query Match 100.0%; Score 444; DB 7; Length 84;
Best Local Similarity 100.0%; Pred. No. 4.4e-47;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWIAQVDPKKTQMGSFRINP 60
Db 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWIAQVDPKKTQMGSFRINP 60

Qy 61 DGSQSVVEVTVPNPKVAHSGF 83
Db 61 DGSQSVVEVTVPNPKVAHSGF 83

RESULT 6
ADD38010
ID ADD38010 standard; protein; 84 AA.
XX AC ADD38010;
XX DT 15-JAN-2004 (first entry)
XX DE Human secreted protein #193.
XX KW human secreted protein; Antiallergic; Antiinflammatory; Antibacterial;
XX KW Anti-HIV; Cytostatic; Immunosuppressive; Hemostatic.
XX OS Homo sapiens;
XX PN WO200290526-A2.
XX XX 14-NOV-2002.
XX PF 19-MAR-2002; 2002WO-US008279.
XX PR 21-MAR-2001; 2001US-0277340P.
XX PR 19-JUL-2001; 2001US-0306171P.
XX PR 13-NOV-2001; 2001US-0331287P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PD

PI Rosen CA, Ruben SM;
XX WPI; 2003-140218/13.
XX PT New human secreted proteins and nucleic acid molecules, useful for
XX PT preparing a diagnostic or pharmaceutical composition for diagnosing or
XX PT treating allergic or asthmatic disorders, or related immediate
XX PT hypersensitivity disorders.
XX PS Claim 1; SEQ ID NO 492; 1323pp; English.
XX CC The present invention relates to an isolated polypeptide or human
XX CC secreted protein. The polypeptides, nucleic acid molecules, antibodies or
XX CC their fragments, and agonists or antagonists that bind are useful for
XX CC preparing a diagnostic or pharmaceutical composition for diagnosing or
XX CC treating allergic or asthmatic disorders. The polypeptide is also useful
XX CC for identifying a binding partner by contacting the polypeptide with a
XX CC binding partner, and determining whether the binding partner increases or
XX CC decreases the activity of the polypeptide. The polypeptides and nucleic
XX CC acid molecules are also useful for detecting, preventing, diagnosing,
XX CC prognosticating, treating or ameliorating inflammatory disorders
XX CC neoplastic diseases, wound healing and disorders of epithelial cell
XX CC proliferation, immune disorders, cardiovascular disorders, blood-related
XX CC disorders, infectious diseases, endocrine disorders, or gastrointestinal
XX CC disorders. The nucleic acids are also useful for chromosome
XX CC identification, radiation hybrid mapping or long-range restriction
XX CC mapping, as molecular weight markers or as hybridization or diagnostic
XX CC probes. The polypeptides and antibodies are useful for providing
XX CC immunological probes for differential identification of the tissues
XX CC immunohistochemistry assays. The present sequence represents a human
XX CC secreted protein.
XX SQ Sequence 84 AA;

Query Match 100.0%; Score 444; DB 7; Length 84;
Best Local Similarity 100.0%; Pred. No. 4.4e-47;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWIAQVDPKKTQMGSFRINP 60
Db 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWIAQVDPKKTQMGSFRINP 60

Qy 61 DGSQSVVEVTVPNPKVAHSGF 83
Db 61 DGSQSVVEVTVPNPKVAHSGF 83

RESULT 7
ADJ46051
ID ADJ46051 standard; protein; 84 AA.
XX AC ADJ46051;
XX DT 06-MAY-2004 (first entry)
XX DE Novel human secreted protein-related protein sequence SeqID204.
XX KW secreted protein; upstream regulator; gene therapy; protein purification;
XX KW protein synthesis; chromosomal mapping; individual identification;
XX KW forensic; hereditary disease; drug reaction; immunoassay;
XX KW epitope mapping; vaccine; immune system regulation;
XX KW haematopoietic system; tissue growth; reproductive hormone;
XX KW cell migration; blood clotting; receptor/ligand interaction;
XX KW adhesion molecule; assisted drug delivery;
XX KW human glial maturation factor gamma-2; neurite outgrowth;
XX KW neurite resprouting; human.
XX OS Homo sapiens.
XX XX US2003144490-A1.
XX PN 31-JUL-2003.
XX PD

```

PF 10-DEC-2002; 2002US-00319763.  
XX 13-NOV-1997; 97US-0066677P.  
PR 17-DEC-1997; 97US-0069957P.  
PR 09-FEB-1998; 98US-0074121P.  
PR 13-APR-1998; 98US-0081563P.  
PR 10-AUG-1998; 98US-0096118P.  
PR 04-SEP-1998; 98US-0099273P.  
PR 13-NOV-1998; 98US-00191997.  
PR 15-SEP-2000; 2000US-00663600.  
XX (EDWA/) EDWARDS J D M.  
PA (DUCL/) DUCLERT A.  
PA (BOUG/) BOUGUELERET L.  
XX Edwards JDM, Duclert A, Bougueleret L;  
XX WPI; 2003-851788/79.  
XX N-PSDB; ADJ46004.  
XX New nucleic acid encoding secreted human polypeptides, useful e.g. in  
PT gene therapy or diagnosis, also encoded proteins, potential therapeutic  
PT agents.  
XX  
XX Claim 11; SEQ ID NO 204; 269pp; English.  
XX  
XX This invention relates to novel purified isolated polynucleotides which  
CC comprise a sequence that encodes at least 10 amino acids (aa) from any of  
CC 48 secreted polypeptide sequences, given in the specification, or  
CC fragments of polypeptides encoded by human cDNA contained in the  
CC corresponding deposited clone. The DNA sequences of the invention encode  
CC secreted proteins (or their fragments) and can be used to  
CC identify/isolate upstream regulators, potentially useful in gene therapy  
CC or protein purification, by controlling protein synthesis, as probes for  
CC chromosomal mapping, identification of individuals, and for diagnosis or  
CC forensics, for example identifying genes associated with hereditary  
CC diseases or drug reactions, for recombinant expression of the encoded  
CC proteins or, where the DNA sequence encodes a signal peptide, for  
CC directing secretion of heterologous polypeptides. Polypeptides encoded by  
CC the DNA sequences of the invention can be used to raise antibodies,  
CC useful for detecting the polypeptide, as (anti)agonists, or for preparing  
CC anti-idiotypic antibodies, as tags in for example immunoassays, epitope  
CC mapping or vaccines, also as molecular weight markers, to screen for  
CC agents with biological activity and as therapeutic agents with,  
CC potentially, a very wide range of activities, for example regulation of  
CC the immune or haematopoietic systems, tissue growth, reproductive  
CC hormones, cell migration, blood clotting or receptor/ligand interaction,  
CC also as adhesion molecules for assisted drug delivery. A typical isolated  
CC sequence is human glial maturation factor gamma-2, which stimulates  
CC neurite outgrowth and resprouting. The present sequence is that of a  
CC human secreted protein of the invention.  
XX  
SQ Sequence 84 AA;  
Query Match 100.0%; Score 444; DB 7; Length 84;  
Best Local Similarity 100.0%; Pred. No. 4.4e-47;  
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKGKWLALLIGALLGTAWARRSQDLHCGACRALVDELEWIAQVDPKKTQMGSFRINP 60  
DB 1 MKGKWLALLIGALLGTAWARRSQDLHCGACRALVDELEWIAQVDPKKTQMGSFRINP 60  
QY 61 DGSQSVVEVTVPNKNVAHSGF 83  
DB 61 DGSQSVVEVTVPNKNVAHSGF 83  
RESULT 8  
ADP19460  
ID ADP19460 standard; protein; 84 AA.  
XX  
AC ADP19460;  
XX

DT 26-AUG-2004 (first entry)  
XX Human secreted polypeptide #311.  
XX Human; secreted protein; genetic disease.  
XX Homo sapiens.  
XX OS  
XX US2004110939-A1.  
XX 10-JUN-2004.  
XX 15-OCT-2001; 2001US-00978360.  
XX 17-DEC-1998; 98WO-IB002122.  
XX 09-FEB-1999; 99WO-IB000282.  
XX 21-JUN-2000; 2000WO-IB000951.  
XX 15-SEP-2000; 2000US-00663600.  
XX (GEST ) GENSET SA.  
XX Dumas Milne Edwards J, Bougueleret L, Jobert S, Clusel C;  
XX Duclert A;  
XX WPI; 2004-440404/41.  
XX N-PSDB; ADP19055.  
XX New isolated polynucleotide encoding secreted polypeptide, useful for  
PT gene therapy, or in diagnostic procedures to identify individuals having  
PT genetic diseases resulting from abnormal expression of the genes.  
XX  
XX Claim 2; SEQ ID NO 716; 113pp; English.  
XX  
XX The invention relates to human cDNA sequences that encode human secreted  
CC proteins. The invention also relates to an antibody that specifically  
CC binds to a polypeptide of the invention and a method of binding the  
CC polypeptide to an antibody. The polynucleotides are useful for expressing  
CC the entire secreted proteins which they encode and for distinguishing  
CC human tissues and cells from non-human tissues and cells, and for  
CC distinguishing between human tissues and cells that do or do not express  
CC the polynucleotides comprising the cDNAs. The polynucleotides and  
CC polypeptides are useful in forensic procedures or diagnostic procedures  
CC to identify individuals with genetic diseases resulting from abnormal  
CC expression of the genes corresponding to the cDNAs. The sequences are  
CC also useful in gene therapy to control or treat genetic diseases. This  
CC sequence represents a human secreted polypeptide of the invention. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 84 AA;  
Query Match 100.0%; Score 444; DB 8; Length 84;  
Best Local Similarity 100.0%; Pred. No. 4.4e-47;  
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKGKWLALLIGALLGTAWARRSQDLHCGACRALVDELEWIAQVDPKKTQMGSFRINP 60  
DB 1 MKGKWLALLIGALLGTAWARRSQDLHCGACRALVDELEWIAQVDPKKTQMGSFRINP 60  
QY 61 DGSQSVVEVTVPNKNVAHSGF 83  
DB 61 DGSQSVVEVTVPNKNVAHSGF 83  
RESULT 9  
AA130716  
ID AA130716 standard; protein; 85 AA.  
XX  
AC AA130716;  
XX  
XX 18-NOV-1999 (first entry)  
XX

Amino acid sequence of a human secreted protein.

Secreted protein; gene therapy; cancer; tumor; fetal deficiency;  
neurodegenerative disorder; developmental abnormality; blood disorder;  
immune system disease; autoimmune disease; leukemia; inflammation;  
allergy; Alzheimer's disease; cognitive disorder; schizophrenia; obesity;  
osteoporosis; arthritis; infection; AIDS; diabetes; asthma;  
connective tissue disorder; transplant rejection; sepsis; acne;  
psoriasis; cardiovascular disorder; reproductive disorder; food additive;  
food preservative; storage capability.  
  
Homo sapiens.  
  
W09943693-A1.  
  
02-SEP-1999.  
  
24-FEB-1999; 99WO-US003939.  
  
26-FEB-1998; 98US-0076051P.  
26-FEB-1998; 98US-0076052P.  
26-FEB-1998; 98US-0076053P.  
26-FEB-1998; 98US-0076054P.  
26-FEB-1998; 98US-0076057P.  
  
(HUMA-) HUMAN GENOME SCI INC.  
  
Olseen HS, Florence K, Brewer LA, Ebner R, Ruben SM, Rosen CA,  
Duan RD;  
  
WPI; 1999-550857/46.  
N-PSDB; AAZ10655.  
  
New human genes and the secreted polypeptides they encode, useful for  
diagnosis and treatment of e.g. cancers, neurological disorders, immune  
diseases, inflammation or blood disorders.  
  
Claim 11; Page 196; 246pp; English.  
  
AAV30701-37 represent human secreted proteins. The polynucleotides and  
their corresponding secreted polypeptides are useful for preventing,  
treating or ameliorating medical conditions, e.g. by protein or gene  
therapy. Pathological conditions can also be diagnosed by determining the  
amount of the new polypeptides in a sample or by determining the presence  
of mutations in the polynucleotide. Specific uses include developing  
products for the diagnosis or treatment of cancer, tumors.  
  
CC neurodegenerative disorders, developmental abnormalities and fetal  
deficiencies, blood disorders, sepsis, diseases of the immune system,  
autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive  
disorders, schizophrenia, obesity, osteoporosis, arthritis, infections,  
AIDS, connective tissue disorders, transplant rejection, diabetes,  
asthma, sepsis, acne, psoriasis, cardiovascular disorders, and  
reproductive disorders. The polypeptides or polynucleotides can also be  
used as food additives or preservatives, such as to increase or decrease  
storage capabilities, fat content, lipid, protein, carbohydrate,  
vitamins, minerals, cofactors or other nutritional components

Sequence 85 AA;

Query Match 100.0%; Score 444; DB 2; Length 85;  
Best Local Similarity 100.0%; Pred. No. 4.4e-47; Indels 0; Gaps 0;  
Matches 83; Conservative 0; Mismatches 0;

Qy 1 MKGNGWLALLGLLGTAWARRSQDLHCACRALVDLEWEIAQVDPKKTIQMGSRINP 60  
| | | | |  
Db 1 MKGNGWLALLGLLGTAWARRSQDLHCACRALVDLEWEIAQVDPKKTIQMGSRINP 60  
| | | | |  
Qy 61 DGSQSVEVTVTVPNNKVAGSGF 83  
| | | | |  
Db 61 DGSQSVEVTVTVPNNKVAGSGF 83  
| | | | |

RESULT 10



PR 18-APR-2003; 2003US-0463700P.  
 PR 18-APR-2003; 2003US-0463708P.  
 PR 18-APR-2003; 2003US-0463716P.  
 PR 18-APR-2003; 2003US-0463732P.  
 PR 02-MAY-2003; 2003US-0467199P.  
 PR 02-MAY-2003; 2003US-0467201P.  
 PR 02-MAY-2003; 2003US-0467203P.  
 PR 02-MAY-2003; 2003US-0467230P.  
 PR 19-MAY-2003; 2003US-0471306P.  
 PR 19-MAY-2003; 2003US-0471336P.  
 PR 22-MAY-2003; 2003US-0472420P.  
 PR 22-MAY-2003; 2003US-0472430P.  
 PR 09-JUN-2003; 2003US-0476609P.  
 PR 09-JUN-2003; 2003US-0476641P.  
 PR 08-JUL-2003; 2003US-0485218P.  
 PR 08-JUL-2003; 2003US-0485223P.  
 PR 08-JUL-2003; 2003US-0485224P.  
 PR 08-JUL-2003; 2003US-0485325P.  
 PR 14-JUL-2003; 2003US-0486446P.  
 PR 14-JUL-2003; 2003US-0486480P.  
 PR 15-JUL-2003; 2003US-0486891P.  
 PR 15-JUL-2003; 2003US-0486960P.  
 PR 08-AUG-2003; 2003US-0493341P.  
 PR 08-AUG-2003; 2003US-0493370P.  
 PR 08-AUG-2003; 2003US-0493573P.  
 PR 08-AUG-2003; 2003US-0493577P.

# (FIVE-) FIVE PRIME THERAPEUTICS INC.

XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;  
 PI Halenbeck RP, Huang MM, Kothakota S, Haishan L, Linnemann T;  
 PI Pierce K, Wang Y, Wong JGF, Wu G, Zhang H;

XX WPI; 2004-348438/32.

DR New nucleic acid molecule for diagnosing, preventing or treating diseases  
 XX such as proliferative (e.g. cancer), inflammatory, immune, metabolic,  
 PT genetic, bacterial and viral diseases.

XX Claim 1; SEQ ID NO 1265; 428pp; English.

XX The present invention relates to an isolated nucleic acid molecule  
 CC encoding a polypeptide which is believed to be cytostatic,  
 CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The  
 CC composition and methods are useful for diagnosing, preventing and  
 CC treating diseases such as proliferative (e.g. cancer), inflammatory,  
 CC immune, metabolic, genetic, bacterial and viral diseases. The present  
 CC sequence represents a human secreted protein. The present sequence is  
 CC available on WIPOMEB and is not in the specification.

XX Sequence 168 AA;

SQ Query Match 83.1%; Score 369; DB 8; Length 168;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-37;  
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGWGLALLIGALLGTAWARRSODLHCGACRALVDELEWEIAQVDPKKTQMGSFRINP 60  
 Db 1 MKGWGLALLIGALLGTAWARRSODLHCGACRALVDELEWEIAQVDPKKTQMGSFRINP 60

Qy 61 DGSQSVVEV 69

Db 61 DGSQSVVEV 69

RESULT 13

AAW88474

ID AAW88474 standard; protein; 182 AA.

XX AAW88474;

AC AAW88474;

XX 10-MAY-1999 (first entry)

XX 10-MAY-1999 (first entry)

DE Human secretory peptide-9 (Zsig9) variaht.

XX Secretory peptide-9; Zsig9; human; tumour marker; cancer; therapy;  
 KW diagnosis; growth enhancer; variant.

XX Homo sapiens.

XX Key Location/Qualifiers

PH Peptide i..20

FT Protein /note= "signal peptide"

FT Protein 21..182

XX /note= "mature protein"

PN WO9901554-A1.

XX 14-JAN-1999.

XX 02-JUL-1998; 98WO-US013859.

XX 03-JUL-1997; 97US-0051704P.

XX 03-JUL-1997; 97US-00888088.

XX 19-MAY-1998; 98US-00081338.

XX 19-MAY-1998; 98US-0085983P.

XX 17-JUN-1998; 98US-00099005.

XX 17-JUN-1998; 98US-0089899P.

XX (ZYMO ) ZYMOGENETICS INC.

XX Sheppard PO, Jelinek LJ, Jaspers SR, Whitmore TE;

XX WPI; 1999-106055/09.

XX N-PSDB; AAX06969.

XX New mammalian secretory peptide-9 (Zsig9) - used as a growth enhancer for

XX placenta, liver and heart, and as an indicator of cancer.

XX Claim 8; Page 74-75; 85pp; English.

XX This is the amino acid sequence of a human secretory peptide-9 (Zsig9)  
 CC variant (see also AAW88469). Zsig9 is overexpressed in human brain,  
 CC liver, lung, oesophageal, stomach, colon, rectal, thyroid and lymphoma  
 CC tumor, and can thus be used as an indicator for cancer. Zsig9 variant  
 CC cDNA is provided in AAX06969. The invention provides Zsig9 polypeptides  
 CC (see AAW88469-77) including mature polypeptides, other processed forms,  
 CC variants and mouse orthologues, and polynucleotides (see AAX06968-70)  
 CC encoding them. Antibodies raised against Zsig9 can be used as diagnostic  
 CC agents to determine the presence of Zsig9, and thus the presence of  
 CC cancer. They can also be labelled with radioisotopes or fused with toxins  
 CC and used to treat tumours which overexpress Zsig9. Antisense nucleotides  
 CC derived from Zsig9 cDNA can also be used to inhibit the growth of tumour  
 CC cells. Zsig9 proteins can be used to enhance the growth or development of  
 CC the placenta, heart or liver

XX Sequence 182 AA;

SQ Query Match 83.1%; Score 369; DB 2; Length 182;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-37;  
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKGWGLALLIGALLGTAWARRSODLHCGACRALVDELEWEIAQVDPKKTQMGSFRINP 60  
 Db 1 MKGWGLALLIGALLGTAWARRSODLHCGACRALVDELEWEIAQVDPKKTQMGSFRINP 60

Qy 61 DGSQSVVEV 69

Db 61 DGSQSVVEV 69

RESULT 14

AAI36200

ID AAY36200 standard; protein; 182 AA.

XX AAY36200;

XX AAY36200;

AC AAY36200;



XX DT 23-SEP-1999 (first entry)  
XX DE Human secreted protein #72.  
XX KW Secreted protein; human; cytostatic; thrombotic; osteopathic; forensic;  
XX KW diagnostic; gene therapy; chromosome mapping; secretion vector.  
XX OS Homo sapiens.  
XX PN W09925825-A2.  
XX PD 27-MAY-1999.  
XX PF 13-NOV-1998; 98WO-IB001862.  
XX PR 13-NOV-1997; 97US-0066677P.  
XX PR 17-DEC-1997; 97US-0069957P.  
XX PR 09-FEB-1998; 98US-0074121P.  
XX PR 13-APR-1998; 98US-0081563P.  
XX PR 10-AUG-1998; 98US-0096116P.  
XX PR 04-SEP-1998; 98US-0099273P.  
XX PA (GEST ) GENSET.  
XX PI Bougueleret L, Duclert A, Dumas Milne Edwards J;  
XX DR WPI; 1999-347472/29.  
XX DR N-PSDB; AAX97884.  
XX PT Extended cDNAs encoding secreted proteins.  
XX PS Claim 7; Page 299; 307pp; English.  
XX CC AAY36129-736222 represent novel human secreted proteins encoded by the  
CC the invention have cytostatic, thrombotic and osteopathic activity. The  
CC extended cDNAs can be used to express secreted proteins or parts of them  
CC or to obtain antibodies capable of binding to the secreted proteins. They  
CC may also be used in diagnostic, forensic, gene therapy and chromosome  
CC mapping procedures. Uses also include design of expression vectors and  
CC secretion vectors  
XX SQ Sequence 182 AA;  
Query Match 83.1%; Score 369; DB 2; Length 182;  
Best Local Similarity 100.0%; Pred. No. 2.5e-37;  
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWIEIAQVDPKTTIQMGSFRINP 60  
Db 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWIEIAQVDPKTTIQMGSFRINP 60  
Qy 61 DGSQSVVEV 69  
Db 61 DGSQSVVEV 69  
RESULT 15  
AAY15135  
ID AAY15135 standard; protein; 182 AA.  
XX AC AAY15135;  
XX DT 07-FEB-2000 (first entry)  
XX DE Human Zsig9 secretory protein variant-4.  
XX KW Secretory protein-9; Human Zsig9; chromosome 12q15 region; variant;  
KW overexpression; antagonist; antibody; antisense nucleotide; tumour;  
KW treatment; receptor; radio-label; fusion; polypeptide toxin; technique;  
KW down-regulation; probe; diagnostic; therapeutic; cancer; liver;  
KW detection; stomach; lymphoma; alternative splicing; allelic variation;

KW silent mutation.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
FT Peptide 1..20  
FT Protein /label= Signal\_sequence  
FT /label= Mature Zsig9 protein variant-4  
FT /note= "Overexpressed in tumours"  
XX PN W09960405-A1.  
XX PD 25-NOV-1999.  
XX PF 19-MAY-1999; 99WO-US011107.  
XX PR 19-MAY-1998; 98US-00081183.  
XX PA (ZYMO ) ZYMOGENETICS INC.  
XX PI Moore EE, Taft DW;  
XX DR WPI; 2000-039447/03.  
XX DR N-PSDB; AAZ08293.  
XX PT Detecting tumors using antibodies, antagonists and antisense nucleotides  
XX PT to secretory protein-9 (Zsig9).  
XX PS Disclosure; Page 35; 45pp; English.  
XX CC The present sequence is a variant of the secretory protein-9, Zsig9 that  
CC arises due to alternative splicing, allelic variation or silent mutations  
CC that result in amino acid changes. This sequence is mapped to the human  
CC chromosome 12q15 region. It is overexpressed in tumours. Antagonists,  
CC antibodies and antisense nucleotides to Zsig9 are useful for detecting  
CC and treating tumours. The antagonist may be an antibody or receptor to  
CC Zsig9 and it may be radio-labelled or fused to a polypeptide toxin. It  
CC can be used for down regulating the overexpression of Zsig9. The gene  
CC sequence can be used as nucleic acid probes to detect RNA encoding Zsig9.  
CC The Zsig9 sequence facilitates improved diagnostic and therapeutic  
CC techniques for detecting and treating cancers, especially of the brain,  
CC liver, stomach, lymphoma etc., at an early stage  
XX SQ Sequence 182 AA;  
Query Match 83.1%; Score 369; DB 3; Length 182;  
Best Local Similarity 100.0%; Pred. No. 2.5e-37;  
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWIEIAQVDPKTTIQMGSFRINP 60  
Db 1 MKGHWLALLGALLGTAWARRSQDLHCGACRALVDELEWIEIAQVDPKTTIQMGSFRINP 60  
Qy 61 DGSQSVVEV 69  
Db 61 DGSQSVVEV 69  
Search completed: May 8, 2006, 20:52:57  
Job time : 189 secs

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 8, 2006, 20:49:59 ; Search time 227 Seconds  
(without alignments)  
257.968 Million cell updates/sec

Title: US-10-716-824-2

Perfect score: 444

Sequence: 1 MKGNGWLALLGALLGTANA.....QSVVEVTVPNNKVAHSGF 83

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	369	83.1	182	1	MSAP_HUMAN	Q9y2b0 homo sapien
2	361	81.3	182	1	MSAP_MOUSE	Q9qxt0 mus musculu
3	253	57.0	184	2	Q6GPD6_XENLA	Q6gpd6 xenopus lae
4	253	57.0	184	2	Q4KLC8_XENLA	Q4klc8 xenopus lae
5	215.5	48.5	184	2	Q4SS46_TETNG	Q4ss46 tetraodon n
6	161.5	36.4	181	2	Q5M7B4_XENLA	Q5m7b4 xenopus lae
7	125.5	28.3	192	2	Q6L1S6_CAEBR	Q6l1s6 caenorhabdi
8	123	27.7	193	2	Q95QX1_CABEL	Q95qnl caenorhabdi
9	96	21.6	189	2	Q3V5F4_DROME	Q9v5f4 drosophila
10	87	19.6	187	2	Q7PPM0_ANOGA	Q7ppm0 anopheles g
11	75.5	17.0	146	2	Q8XVW7_RALSTO	Q8xvw7 ralstonia s
12	75.5	17.0	327	2	Q87K51_SYMTH	Q87k51 symbiobacte
13	74	16.7	299	2	Q94RE3_LITFO	Q94re3 lithobius f
14	72.5	16.3	377	1	PGES2_HUMAN	Q9h7z7 homo sapien
15	71.5	16.1	238	2	Q7Q4F3_ANOGA	Q7q4f3 anopheles g
16	71.5	16.1	335	2	Q9SM22_VANPL	Q9sm22 vanilla pla
17	70.5	15.9	375	2	Q7TXS8_MYCBO	Q7txs8 mycobacteri
18	70.5	15.9	375	2	P16333_MYCCTU	P16333 mycobacteri
19	70.5	15.9	384	1	PGES2_MOUSE	Q8bwm0 mus musculu
20	70.5	15.9	595	2	Q5EK30_VIBCH	Q5ek30 vibrio chol
21	70.5	15.9	731	2	Q7UQK4_RHOBA	Q7uqk4 rhodopirell
22	70	15.8	353	2	Q7QTC5_GIALA	Q7qtc5 giardia lam
23	70	15.8	1871	2	Q8MT99_GIALA	Q8mt99 giardia lam
24	69.5	15.7	168	2	Q8T512_TABSO	Q8t512 taenia soli
25	69.5	15.7	566	2	Q926R8_LISIN	Q926r8 listeria in
26	69	15.5	181	2	Q9I148_PSEAE	Q9i148 pseudomonas
27	69	15.5	291	2	Q5KZL8_GEOKA	Q5kzl8 geobacillus
28	69	15.5	593	2	Q9FJ00_ARATH	Q9fjq0 arabidopsis
29	68.5	15.4	152	2	Q9W4C2_DROME	Q9w4c2 drosophila
30	68	15.3	150	2	Q7U2B4_RHOBA	Q7u2b4 rhodopirell
31	68	15.3	162	2	Q9KMZ3_VIBCH	Q9kmz3 vibrio chol

32 68 15.3 311 2 Q9G3Z6\_LITFO Q9g3z6 lithobius f  
33 68 15.3 789 2 Q5F3L1\_CHICK Q5f3l1 gallus gall  
34 68 15.3 821 2 Q4RTV2\_TETNG Q4rtv2 tetraodon n  
35 67.5 15.2 236 2 Q5QY25\_IDIOMA Q5qy25 idiomarina  
36 67.5 15.2 337 2 Q8S2S0\_THEHA Q8s2s0 thellungiel  
37 67.5 15.2 377 1 PGES2\_MACFA PGes2 macaca faec  
38 67.5 15.2 413 2 Q8Y3J5\_LISTER Q8y3j5 listeria mo  
39 67.5 15.2 566 2 Q7IVS1\_LISMF Q7ivs1 listeria mo  
40 67.5 15.2 616 2 Q5B1F2\_EMENI Q5b1f2 aspergillus  
41 67 15.1 105 2 Q5E184\_9VIRU Q5e184 potato mop-  
42 67 15.1 106 2 Q5E186\_9VIRU Q5e186 potato mop-  
43 67 15.1 312 2 Q5LEH7\_BACFN Q5leh7 bacteroides  
44 67 15.1 440 2 Q8LUF5\_BACAN Q8luf5 bacillus an  
45 67 15.1 1243 2 Q53MF0\_ORYSA Q53mf0 oryza sativ

#### ALIGNMENTS

RESULT 1  
ID \_MSAP\_HUMAN STANDARD; PRT; 182 AA.  
AC Q9Y2B0; Q9UHE9;  
DT 25-OCT-2004 (Rel. 45, Created)  
DT 25-OCT-2004 (Rel. 45, Last sequence update)  
DE MIR-interacting saposin-like protein precursor (Transmembrane protein  
4) (Putative secreted protein ZSIGN9).  
GN Name=TMEM4; Synonym=MSAP, ZSIGN9; ORFNAMES=UNQ1943/PRO4426;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).  
RC TISSUE=Gastric adenocarcinoma;  
RX MEDLINE=99173880; PubMed=10072769; DOI=10.1016/S0378-1119(99)00004-9;  
RA Yokoyama-Kobayashi M., Yamaguchi T., Sekine S., Kato S.;  
RT "Selection of cDNAs encoding putative type II membrane proteins on the  
cell surface from a human full-length cDNA bank.";  
RL Gene 228:161-167(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE (ISOFORM 1), INTERACTION WITH MYLIP, AND TISSUE  
SPECIFICITY.  
RX PubMed=12826659; DOI=10.1074/jbc.M306271200;  
RA Bornhauser B.C., Olsson P.-A., Lindholm D.;  
RT "MSAP is a novel MIR-interacting protein that enhances neurite  
outgrowth and increases myosin regulatory light chain.";  
RL J. Biol. Chem. 278:35412-35420(2003).  
RN [3]  
RP NUCLEOTIDE SEQUENCE (ISOFORM 2).  
RA Sheppard P., Jelinek L., Whitmore T., Blumberg H., Lehner J.,  
O'Hara P.;  
RT "Homo sapiens putative secreted protein.";  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,  
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
Eaton D., Fother J.S., Grimaldi C., Gu Q., Hass P.E., Heidens S.,  
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,  
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
Vandlen R.L., Watanabe C., Wleand D., Woods K., Xie M.-H.,  
Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,  
Wood W.I., Godowski P.J., Gray A.M.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
effort to identify novel human secreted and transmembrane proteins: a  
bioinformatics assessment.";  
RL Genome Res. 13:2265-2270(2003).  
RN [5]



RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Maria M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
CC -1- FUNCTION: Positive regulator of neurite outgrowth (By similarity).  
CC -1- SUBUNIT: Interacts with MYLIP/MIR (By similarity).  
CC -1- SIMILARITY: Contains 1 saposin B-type domain.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use as long as its content is in no way modified and this statement is not  
removed.  
CC -----  
CC EMBL; AF186115; AAF01433.1; -; mRNA.  
CC EMBL; AK007914; BAB25346.1; -; mRNA.  
CC EMBL; AK013014; BAB28597.1; -; mRNA.  
CC EMBL; AK013568; BAB28909.1; -; mRNA.  
CC EMBL; AK019927; BAB31921.1; -; mRNA.  
CC EMBL; BC008261; AAH08261.1; -; mRNA.  
CC Ensembl; ENSMUSG0000025381; Mus musculus.  
CC MGI; MGI-1928477; Tmem4.  
CC GO; GO:0005615; C:extracellular space; TAS.  
CC InterPro; IPR00886; ER target\_S.  
CC InterPro; IPR008139; SaposinB.  
CC PROSITE; PS00014; ER\_TARGET; 1.  
CC PROSITE; PS50015; SAP\_B; 1.  
CC Signal.  
CC SIGNAL 1 20 Potential.  
CC CHAIN 21 182 MIR-interacting saposin-like protein.  
CC DOMAIN 24 175 Saposin B-type.  
CC MOTIF 179 182 Prevents secretion from ER (Potential).  
CC SEQUENCE 182 AA; 20767 MW; 83E54E7F01E9B87 CRC64;  
Query Match 81.3%; Score 361; DB 1; Length 182;  
Best Local Similarity 97.1%; Pred. No. 2.9e-31;  
Matches 67; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MKGNGWLLALLGLGTAWARRSODLHCGACRALVDELEWEIAQVDPKKTQMGSPRNP 60  
Db 1 MKGNGWLLALLGLGTAWARRSODLHCGACRALVDELEWEIAQVDPKKTQMGSPRNP 60  
Qy 61 DGSQSVVEV 69  
Db 61 DGSQSVVEV 69  
RESULT 3  
Q6GPD6\_XENLA  
ID Q6GPD6\_XENLA PRELIMINARY; PRT; 184 AA.  
AC Q6GPD6\_XENLA  
DT 08-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE MG80474 protein.  
GN Name=MG80474;  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodinae; Xenopus; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Maria M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Embryo;  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
initiative";  
RL Dev. Dyn. 225:384-391 (2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Embryo;  
RA Klein S., Gerhard D.S.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC073204; AAH73204.1; -; mRNA.  
DR InterPro; IPR00886; ER\_target\_S.  
DR InterPro; IPR008139; SaposinB.  
DR PROSITE; PS00014; ER\_TARGET; UNKNOWN 1.  
SQ SEQUENCE 184 AA; 21039 MW; 1BDED5D398918E3E CRC64;  
Query Match 57.0%; Score 253; DB 2; Length 184;  
Best Local Similarity 74.6%; Pred. No. 2e-19;  
Matches 47; Conservative 9; Mismatches 7; Indels 0; Gaps 0;  
Qy 6 WLALLGALLGTAWARRSODLHCGACRALVDELEWEIAQVDPKKTQMGSPRNP 65  
Db 10 FLPIVLVSLVGYVCARRGQDVHCGACRALVDELEWEISQVDPKKTQMGSPRNP 69  
Qy 66 VVE 68  
Db 70 VIE 72  
RESULT 4  
Q4KLC8\_XENLA  
ID Q4KLC8\_XENLA PRELIMINARY; PRT; 184 AA.  
AC Q4KLC8\_XENLA  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RA Klein S., Gerhard D.S.;
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC099289; AA099289.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 184 AA; 21007 MW; CCB7184926917596 CRC64;

Query Match 57.0%; Score 253; DB 2; Length 184;
Best Local Similarity 73.4%; Pred. No. 2e-19;
Matches 47; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 6 WLALLGALLGTAWARRSQDLHCACRALVDELEWEIAQVDPKKTQMGSRINPDGQS 65
Db 10 FLPIVLVSLGCVCARRGQDVHCACRALVDELEWEISQVDPKKTQKGSFHINPDGQS 69

Qy 66 VVEV 69
Db 70 VIEV 73

RESULT 5
Q4SS46.TETNG PRELIMINARY; PRT; 184 AA.
AC Q4SS46;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 11 SCAP14479, whole genome shotgun sequence.
GN ORFNames=GSTENG0001361400;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot N.,
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot N.,

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RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dosat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Bremond C., Skalll Z., Cattolico L., Poutain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crollius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CA001014479; CAF96536.1; -; Genomic DNA.
SQ SEQUENCE 184 AA; 20614 MW; 89CE0010ED99D9B9 CRC64;

Query Match 48.5%; Score 215.5; DB 2; Length 184;
Best Local Similarity 71.9%; Pred. No. 2.5e-15;
Matches 46; Conservative 6; Mismatches 9; Indels 3; Gaps 2;

Qy 8 ALLLGALL--GTAWARRSQDLHCACRALVDELEWEIAQVDPKKTQMGSRINPDGQS 65
Db 11 SLLLFLLSPGQA-ARQGDMKCGACRALVDELEWEIAISQVDPKKTQMGSRINPDGQS 69

Qy 66 VVEV 69
Db 70 IREV 73

RESULT 6
Q5M7D4.XENLA
ID Q5M7D4.XENLA PRELIMINARY; PRT; 181 AA.
AC Q5M7D4;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE LOC496234 protein.
GN Name=LOC496234;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA Klein S., Gerhard D.S.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC088697; AAH8697.1; -; mRNA.
DR InterPro; IPR000886; ER target S.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN 1.
SQ SEQUENCE 181 AA, 20706 MW, B2B8641C5413F924 CRC64;

Query Match 36.4%; Score 161.5; DB 2; Length 181;
Best Local Similarity 54.5%; Pred. No. 2e-09;
Matches 36; Conservative 12; Mismatches 9; Indels 9; Gaps 3;

QY 7 LALLL--GALLGTAW-----ARSDLHCGACALVDELEWEIAQVDPKKTQMGSFRI 58
DB 1 MAILLHFGVLI-TAFLLSHVEGRDPILYCGACALVDELLYEIRKNPKKTVDVGSFRI 59
QY 59 NPDGSQ 64
DB 60 SPDGKQ 65

RESULT 7
Q61L56 CAEBR
ID Q61L56 CAEBR PRELIMINARY; PRT; 192 AA.
AC Q61L56;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG09065.
GN Names=CBG09065;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAC0100041; CAB64378.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 192 AA, 21152 MW, 619ADEC09CB411D5 CRC64;

Query Match 28.3%; Score 125.5; DB 2; Length 192;
Best Local Similarity 50.0%; Pred. No. 1.9e-05;
Matches 28; Conservative 8; Mismatches 19; Indels 1; Gaps 1;

QY 9 LLLGALLGTAWRRSDPLHCGACALVDELEWEIAQVDPKKTQMGSFRIINPDGSQ 64
DB 9 ILLSSIGFNSASVS-SLECCAGCSLLVTHFELKIAVDPPKKIEVGSFRVSPGTGEQ 63

RESULT 8
Q95QN1 CAEBL
ID Q95QN1 CAEBL PRELIMINARY; PRT; 193 AA.
AC Q95QN1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

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DE Hypothetical protein F01F1.15.
GN ORFNames=F01F1.15;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequencing of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; U13070; AK67223.1; -; Genomic DNA.
DR Ensemble; F01F1.15; Caenorhabditis elegans.
DR WormBase; WBGene00017169; F01F1.15.
DR WormPep; F01F1.15; CE26884.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 193 AA, 21112 MW, 072306588AF3C067 CRC64;

Query Match 27.7%; Score 123; DB 2; Length 193;
Best Local Similarity 59.0%; Pred. No. 3.5e-05;
Matches 23; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 26 LHCGACALVDELEWEIAQVDPKKTQMGSFRIINPDGSQ 64
DB 24 LECCAGCSLLVTHFELKIAVDPPKKIEVGSFRVSPGTGDQ 62

RESULT 9
Q9V5F4 DROME
ID Q9V5F4 DROME PRELIMINARY; PRT; 189 AA.
AC Q9V5F4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE CG12918-PA (GH10427p).
GN ORFNames=CG12918;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananthakrishnan P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt J., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harries N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Neison D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chanderlin M., Choise N., Claudel-Renard C., Cunac S., Damange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguer P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646071; CAD16417.1; -; Genomic_DNA.
KW Complete proteome; Lipoprotein.
SQ SEQUENCE 146 AA; 15350 MW; 784620C8F060D589 CRC64;

Query Match 17.0%; Score 75.5; DB 2; Length 146;
Best Local Similarity 28.6%; Pred. No. 4.2;
Matches 22; Conservative 14; Mismatches 28; Indels 13; Gaps 3;

Oy 6 WLALLGALLGTAWARRSQDLHCACRALVDELEWEIAQVDPKKTQMGSPRINPDGSGS 65
Db 8 WTAALMG-LGVCAIAAQDIPVGTCRPMVGQ-----AEIDGVMOQVSGTACLOPDGTWQ 60

Oy 66 VVEVTVTVPKNAHSG 82
Db 61 MADGTT-----VAYAG 71

RESULT 12
O67K51_SYNTH
ID O67K51_SYNTH PRELIMINARY; PRT; 327 AA.
AC O67K51;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Cation efflux system protein.
GN OrderedLocustNames=STH2964;
OS Symbiobacterium thermophilum.
OC Bacteria; Actinobacteria; Symbiobacterium.
OX NCBI_TaxID=2734;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IAM14863;
RX PubMed=15383646; DOI=10.1093/nar/gkh830;
RA Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,
RA Morimura K., Ikeda H., Hattori M., Beppu T.;
RT "Genome sequence of Symbiobacterium thermophilum, an uncultivable bacterium that depends on microbial commensalism.";
RL Nucleic Acids Res. 32:4937-4944(2004).
DR EMBL; AP006840; BAD41947.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008324; P:cation transporter activity; IEA.
DR GO; GO:0006812; P:cation transporter activity; IEA.
DR InterPro; IPR002524; C:cation efflux; IEA.
DR Pfam; PF01545; C:cation efflux; 1.
DR TIGRFAMs; TIGR01297; CDF; 1.
KW Complete proteome.
SQ SEQUENCE 327 AA; 34193 MW; 3E1CD40918B6097B CRC64;

Query Match 17.0%; Score 75.5; DB 2; Length 327;
Best Local Similarity 35.8%; Pred. No. 9.7;
Matches 29; Conservative 9; Mismatches 32; Indels 11; Gaps 4;

Oy 3 GWG-----LALLGALLG-TAWARRSQDLHC-----GACRALVDELEWEIAQVDPKKTQ 53
Db 208 GWRWADPLAGLTVAAALRTARTAWSITGSEAAHMLMDGFADRARIAALEEVVLGVQGVTVGQ- 266

Oy 54 GSFRINPDGSGSVVEVTVP 74
Db 267 -SLRRLMGSRVHDVTVLVP 286

RESULT 13
O94RE3_LITFO
ID O94RE3_LITFO PRELIMINARY; PRT; 299 AA.
AC O94RE3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE NADH dehydrogenase subunit 1.
GN Name=ND1;
OS Lithobius forficatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda;
OC Pleurostigmophora; Lithobiomorpha; Lithobiidae; Lithobius.
OX NCBI_TaxID=7552;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21441907; PubMed=11557978; DOI=10.1038/35093090;
RA Hwang U., Friedrich M., Choe C., Kim W.;
RT "Mitochondrial protein phylogeny joins myriapods with chelicerates.";
RL Nature 413:154-157(2001).
DR EMBL; AJ270997; CAC69948.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR001694; P:electron transport; IEA.
DR Pfam; PF00146; NADHdh; 1.
DR PROSITE; PS00667; COMPLEX1_ND1_1; 1.
KW Mitochondrion.
SQ SEQUENCE 299 AA; 33719 MW; 0927CDD757ED7878 CRC64;

Query Match 16.7%; Score 74; DB 2; Length 299;
Best Local Similarity 28.6%; Pred. No. 13;
Matches 18; Conservative 15; Mismatches 24; Indels 6; Gaps 2;

Oy 3 GW-----GWLALLGALLGTAWARRSQDLHCACRALVDELEWEI--AQVDPKKTQMGSP 56
Db 98 GWLYFLSFIAVSVAIIGSGWFSNKAALLGALRAVAQTISYEVCALMWIIMLVSVGSF 157

Oy 57 RIN 59
Db 158 NLN 160

RESULT 14
PGES2_HUMAN
ID PGES2_HUMAN STANDARD; PRT; 377 AA.
AC Q9H727; Q53EW9; Q5SIV6; Q96G10; Q96GL2;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Prostaglandin E synthase-2 (EC 5.3.99.3) (Microsomal prostaglandin E synthase-2) (mPGES-2) [Contains: Prostaglandin E synthase-2, truncated form].
DE form].
GN Name=PTGES2; Synonyms=PGES2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Embryo;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,

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RA Yamazaki M., Ninomiya K., Ishibaishi T., Yamashita H., Murakawa K.,  
RA Fujimori K., Tanai H., Kinata M., Watanabe M., Hiraoka S., Chiba Y.,  
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hota T.,  
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,  
RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,  
RA Inoue N., Muraahino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,  
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,  
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
RA Fujimori Y., Komiya M., Tashiro H., Tanigami A., Fujiwara T.,  
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,  
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Komatsu T.,  
RA Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,  
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,  
RT "Complete sequencing and characterization of 21,243 full-length human  
RT cDNAs.";  
RL Nat. Genet. 36:40-45(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX PubMed:15164053; DOI=10.1038/nature02465;  
RA Humphray S.J., Oliver K., Hunt A.R., Plumb R.W., Loveland J.E.,  
RA Howe K.L., Andrews T.D., Searle S., Hunt S.E., Scott C.E., Jones M.C.,  
RA Ainscough R., Almeida J.P., Ambrose K.D., Ashwell R.I.S.,  
RA Babbage A.K., Babbage S., Baguley C.L., Bailey J., Banerjee R.,  
RA Barker D.J., Barlow K.P., Bates K., Beasley H., Beasley O., Bird C.P.,  
RA Bray-Allen S., Brown A.J., Brown J.Y., Burford D., Burrill W.,  
RA Burton J., Carder C., Carter N.P., Chapman J.C., Chen Y., Clarke G.,  
RA Clark S.Y., Clee C.M., Clegg S., Collier R.E., Corby N., Crosier M.,  
RA Cummings A.T., Davies J., Dhani P., Dunn M., Dutta I., Dyer L.W.,  
RA Earthrowl M.E., Faulkner L., Fleming C.J., Frankish A.,  
RA Frankland J.A., French L., Fricker D.G., Garner P., Garnett J.,  
RA Ghori J., Gilbert J.G.R., Gleson C., Grafham D.V., Gribble S.,  
RA Griffiths C., Griffiths-Jones S., Grocock R., Guy J., Hall R.E.,  
RA Hammond S., Harley J.L., Harrison E.S.I., Hart E.A., Heath P.D.,  
RA Henderson C.D., Hopkins B.L., Howard P.J., Howden P.J., Huckle E.,  
RA Johnson C., Johnson D., Joy A.A., Kay M., Keenan S., Kershaw J.K.,  
RA Kimberley A.M., King A., Knights A., Laird G.K., Langford C.,  
RA Lawlor S., Leongamornlert D.A., Leverisha M., Lloyd C., Lloyd D.M.,  
RA Lovell J., Martin S., Mashreghi-Mohammadi M., Matthews L., McLaren S.,  
RA McLay K.E., McMurray A., Milne S., Nickerson T., Niebett J.,  
RA Nordsiek G., Pearce A.V., Peck A.I., Porter K.M., Pandian R.,  
RA Pelan S., Phillimore B., Povey S., Ramsey Y., Rand V., Scharfe M.,  
RA Seward H.K., Showkneen R., Sims S.K., Skuce C.D., Smith M.,  
RA Steward C.A., Svarbreck D., Sycamore N., Tester J., Thorpe A.,  
RA Tracey A., Tromans A., Thomas D.W., Wall M., Wallis J.M., West A.P.,  
RA Whitehead S.L., Wiley D.L., Williams S.A., Wilming L., Wray P.W.,  
RA Young L., Ashurst J.L., Coulson A., Blocker H., Durbin R.,  
RA Sulston J.E., Hubbard T., Jackson M.J., Bentley D.R., Beck S.,  
RA Rogers J., Dunham I.;  
RT "DNA sequence and analysis of human chromosome 9.";  
RL Nature 429:369-374(2004).  
RN [4]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Brain and Lung;  
RX PubMed:22388257; PubMed:12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,  
RA Fahay J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalak U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; and  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [5]  
RP TISSUE SPECIFICITY.  
RX PubMed:11866447; DOI=10.1006/bbr.2002.6531;  
RA Tanikawa N., Ohmiya Y., Ohkubo H., Hashimoto K., Kangawa K.,  
RA Kojima M., Ito S., Watanabe K.;  
RT "Identification and characterization of a novel type of membrane-  
RT associated prostaglandin E synthase.";  
RL Biochem. Biophys. Res. Commun. 291:884-889(2002).  
RN [6]  
RP COFACTOR, AND MUTAGENESIS OF CYS-110 AND CYS-113.  
RX PubMed:12804604;  
RA Watanabe K., Ohkubo H., Niwa H., Tanikawa N., Koda N., Ito S.,  
RA Ohmiya Y.;  
RT "Essential 110Cys in active site of membrane-associated prostaglandin  
RT E synthase-2.";  
RL Biochem. Biophys. Res. Commun. 306:577-581(2003).  
RN [7]  
RP CLEAVAGE, AND SUBCELLULAR LOCATION.  
RX PubMed:12835322; DOI=10.1074/jbc.M305108200;  
RA Murakami M., Nakaehima K., Kamei D., Masuda S., Ishikawa Y., Ishii T.,  
RA Ohmiya Y., Watanabe K., Kudo I.;  
RT "Cellular prostaglandin E2 production by membrane-bound prostaglandin  
RT E synthase-2 via both cyclooxygenases-1 and -2.";  
RL J. Biol. Chem. 278:37937-37947(2003).  
RN [8]  
RP INTERACTION WITH EXOSC10.  
RX PubMed:15231747; DOI=10.1101/gr.2122004;  
RA Lehner B., Sanderson C.M.;  
RT "A protein interaction framework for human mRNA degradation.";  
RL Genome Res. 14:1315-1323(2004).  
CC -1- FUNCTION: Isomerase that catalyzes the conversion of unstable  
CC intermediate of prostaglandin E2 H2 (PGH2) into the more stable  
CC prostaglandin E2 (PGE2) form. May also have transactivation  
CC activity toward IFN-gamma (IFNG), possibly via an interaction with  
CC CEBPB; however, the relevance of transcription activation activity  
CC remains unclear.  
CC -1- CATALYTIC ACTIVITY: (5Z,13E)-(15S)-9-alpha,11-alpha-epidioxo-15-  
CC dihydroxyprosta-5,13-dienoate = (5Z,13E)-(15S)-11-alpha,15-  
CC dihydroxy-9-oxoprost-5,13-dienoate.  
CC -1- COFACTOR: dihydroliipoic acid.  
CC -1- PATHWAY: Prostaglandin biosynthesis.  
CC -1- SUBUNIT: Homodimer. May interact with CEBPB (By similarity).  
CC -1- SUBCELLULAR LOCATION: Membrane-bound and soluble. Synthesized as a  
CC Golgi membrane-bound protein, which is further cleaved into the  
CC predominant soluble truncated form. The truncated form is  
CC cytoplasmic and is enriched in the perinuclear region.  
CC -1- TISSUE SPECIFICITY: Widely expressed. Expressed in the heart,  
CC including apex, inter-ventricular septum, both atria and  
CC ventricles, but not in the aorta. Also expressed in fetal heart.  
CC Detected in various regions of the brain: cerebellum; occipital,  
CC frontal and parietal lobes. Also expressed in the lymph nodes,  
CC skeletal muscle, kidney and trachea, but not in the thymus or  
CC lung. Overexpressed in colorectal cancer.  
CC -1- SIMILARITY: Belongs to the GST superfamily.  
CC -1- CAUTION: Ref.3 (CA113822) sequence differs from that shown due to  
CC erroneous gene model prediction.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its

1. The first step is to identify the problem or question that needs to be answered. This involves understanding the context and the specific requirements of the task.

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 8, 2006, 20:53:15 ; Search time 38 Seconds  
(without alignments)  
210.158 Million cell updates/sec

Title: US-10-716-824-2  
Perfect score: 444  
Sequence: 1 MKGWGLALLGLGTAWA.....QSVVEVTVTVPNNKVAHSGF 83

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123	27.7	580	2 T15949	hypothetical prote
2	70.5	15.9	375	2 F70691	hypothetical prote
3	69.5	15.7	566	2 A1803	Sucrose phosphoryl
4	69	15.5	181	2 E83342	hypothetical prote
5	68	15.3	162	2 F82493	hypothetical prote
6	67.5	15.2	377	2 JC7977	membrane-associate
7	67.5	15.2	413	2 AG1429	Sucrose phosphoryl
8	65.5	14.8	233	2 A96495	unknown protein [i
9	65.5	14.8	1040	1 A38306	alpha-mannosidase
10	64.5	14.5	185	2 G84341	hypothetical prote
11	64.5	14.5	325	2 T11116	NADH2 dehydrogenas
12	63.5	14.3	322	2 S01499	NADH2 dehydrogenas
13	63.5	14.3	323	2 T11793	NADH2 dehydrogenas
14	63.5	14.3	323	2 A34284	NADH2 dehydrogenas
15	63.5	14.3	335	2 C96607	probable galactino
16	63.5	14.3	425	2 F83990	lactose transport
17	63.5	14.3	528	2 T10622	hypothetical prote
18	63	14.2	293	2 C90946	heat shock protein
19	63	14.2	293	2 C90946	heat shock protein
20	63	14.2	754	2 S75113	catalase (EC 1.11.
21	63	14.2	3175	1 RRMVSV	genome polypeptin
22	62.5	14.1	151	2 T34640	probable integral
23	62.5	14.1	308	2 A82359	hypothetical prote
24	62	14.0	98	2 S03386	antigen (clone 22)
25	62	14.0	281	2 G87451	hypothetical prote
26	62	14.0	293	2 AD0728	heat shock protein
27	62	14.0	440	2 T15352	hypothetical prote
28	62	14.0	877	2 I48967	brain-specific kin
29	62	14.0	893	2 S51603	receptor-like tyro

30 62 14.0 898 2 S47489 receptor tyrosine  
31 62 14.0 981 2 S51604 receptor-like tyro  
32 62 14.0 1005 2 S49015 receptor tyrosine  
33 61.5 13.9 216 2 C75403 hypothetical prote  
34 61 13.7 175 2 B56745 microfibril-associ  
35 61 13.7 357 2 C86363 Jun activation dom  
36 61 13.7 357 2 T52180 constitutive photo  
37 61 13.7 1040 1 T46931 alpha-mannosidase  
38 61 13.7 1801 2 T26774 hypothetical prote  
39 60.5 13.6 271 2 JT0750 water channel prot  
40 60.5 13.6 296 2 T23239 hypothetical prote  
41 60.5 13.6 387 1 S52274 transcription term  
42 60.5 13.6 407 2 T28795 hypothetical prote  
43 60.5 13.6 813 2 AH3258 cation-transportin  
44 60 13.5 238 1 QOECPE tRNA nucleotidyltr  
45 60 13.5 254 2 B75052 coenzyme pqg synth

ALIGNMENTS

RESULT 1

T15949

hypothetical protein F01F1.11 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 24-Nov-1999

C/Accession: T15949

R/Miller, N.

submitted to the EMBL Data Library, July 1995

A/Description: The sequence of C. elegans cosmid F01F1.

A/Reference number: Z18435

A/Accession: T15949

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-580 <MTL>

A/Cross-references: UNIPARC:UPI0000179068; EMBL:U13070; NID:G529697; PID:G529708; PIDN:G

A/Experimental source: strain Bristol N2

C/Genetics:

A/Gene: CESP:F01F1.11

A/Introns: 66/1; 144/3; 199/3; 269/1; 330/2; 387/2; 415/1; 481/3; 514/3

C/Superfamily: Caenorhabditis elegans hypothetical protein F01F1.11

Query Match 27.7%; Score 123; DB 2; Length 580;

Best Local Similarity 59.0%; Pred. No. 8.5e-06;

Matches 23; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 26 LHCACRALVDELEWEIAQVDPKKTQMGSGFRINPDGSG 64

Db 411 LECGACSLLVTHFELKIAVDPKKKIEVGSFRVSGTGDQ 449

RESULT 2

F70691

hypothetical protein Rv2819c - Mycobacterium tuberculosis (strain H37Rv)

C/Species: Mycobacterium tuberculosis

C/Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004

C/Accession: F70691

R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.

Rajandream, M.A.; Rogers, R.; Rutter, J.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A/Reference number: A70500; MUID:98295987; PMID:9634230

A/Accession: F70691

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-375 <COL>

A/Cross-references: UNIPROT:P71633; UNIPARC:UPI000000D0F90; GB:Z81331; GB:AL123456; NID:G

A/Experimental source: strain H37Rv

C/Genetics:

A/Gene: Rv2819c



Db 120 LDFHALPYQVVEVNPVLRABIKFSSYRKVPILVAQEGSSQQLNDSSVII 169

RESULT 7  
AG1429  
Sucrose phosphorylase homolog lmo2840 [imported] - Listeria monocytogenes (strain EGD-e)  
C;Species: Listeria monocytogenes  
C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 05-Oct-2004  
C;Accession: AG1429  
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blockerx  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A;Authors: Krefft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma  
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,  
A;Title: Comparative genomics of Listeria species.  
A;Reference number: AB1077; MUID:21537279; PMID:11679669  
A;Accession: AG1429  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-413 <GLA>  
A;Cross-references: UNIPROT:Q8Y3J5; UNIPARC:UPI000000CF250; GB:NC\_003210; PIDN:CAD01053.1  
A;Experimental source: strain EGD-e  
C;Genetics:  
A;Gene: lmo2840  
C;Superfamily: sucrose phosphorylase

Query Match 15.2%; Score 67.5; DB 2; Length 413;  
Best Local Similarity 45.0%; Pred. No. 9.8;  
Matches 18; Conservative 6; Mismatches 7; Indels 9; Gaps 1;

Qy 33 ALVDELEWEIAQVDPKKTQMGSPRINPDGSQSVVEVTVT 72  
|||:||||| :|||:||||| :|||  
Db 201 ALVNDLSEEGALV-----SYKQNPDGSKSPYEINVT 231

RESULT 8  
A96495  
unknown protein [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: A96495  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: A96495  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-233 <STO>  
A;Cross-references: UNIPROT:Q9C8E9; UNIPARC:UPI000000A96F7; GB:AE005173; NID:g11141996; H  
C;Genetics:  
A;Gene: T8D8.4  
A;Map position: 1

Query Match 14.8%; Score 65.5; DB 2; Length 233;  
Best Local Similarity 33.3%; Pred. No. 8.9;  
Matches 14; Conservative 10; Mismatches 17; Indels 1; Gaps 1;

Qy 23 SODLHCACRALVDELEWEIAQVDPKKTQMGSPRINPDGSQ 64  
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Db 20 SVDDKCAACNAVABELEQLLKEKPRNHLDMRN-RLMSKGQR 60

RESULT 9  
A38306

alpha-mannosidase (EC 3.2.1.24) - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004  
C;Accession: A38306  
R;Bischhoff, J.; Moremen, K.; Lodish, H.F.  
J. Biol. Chem. 265, 17110-17117, 1990  
A;Title: Isolation, characterization, and expression of cDNA encoding a rat liver endopl  
A;Reference number: A38306; MUID:91009139; PMID:2211613  
A;Accession: A38306  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1040 <BIS>  
A;Cross-references: UNIPROT:P21139; UNIPARC:UPI0000012EAC9; GB:M57547; GB:J05632; NID:g20  
C;Superfamily: Saccharomyces alpha-mannosidase  
C;Keywords: glycosidase; hydrolase

Query Match 14.8%; Score 65.5; DB 1; Length 1040;  
Best Local Similarity 32.0%; Pred. No. 44;  
Matches 24; Conservative 3; Mismatches 25; Indels 23; Gaps 3;

Qy 28 CGACRALVDELEWEIAQVDPKKTQMGSPRINPDGSQ-----SVVEVTVT 72  
|||:||||| :|||:||||| :|||  
Db 386 CGIKRFLTKLSWNLVNSPPHTF----FWEGLDGSQVLVHFPFGDSYGMQGSVEEVLT 441

Qy 73 VPPN-----KVAHSGF 83  
|||:||||| :|||  
Db 442 VTNRDKGRTNHSGF 456

RESULT 10  
G84341  
hypothetical protein Vng1906h [imported] - Halobacterium sp. NRC-1  
C;Species: Halobacterium sp. NRC-1  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: G84341  
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Herquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.  
; Leithauser, B.; Keller, K.; Cruz, R.; Danison, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon  
Jung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li  
A;Title: Genome sequence of Halobacterium species NRC-1.  
A;Reference number: A84160; MUID:20504483; PMID:11016950  
A;Accession: G84341  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-185 <STO>  
A;Cross-references: UNIPROT:Q9HNK1; UNIPARC:UPI00000639D1; GB:AE004437; NID:g10581348; P  
C;Genetics:  
A;Gene: VNG1906H  
C;Superfamily: Escherichia coli hypothetical protein b4140

Query Match 14.5%; Score 64.5; DB 2; Length 185;  
Best Local Similarity 25.3%; Pred. No. 9;  
Matches 22; Conservative 13; Mismatches 33; Indels 19; Gaps 3;

Qy 5 GW-----LALLGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKT-----IQ 52  
|||:||||| :|||:||||| :|||  
Db 30 GWQLTVALVLTALLGLTFVRAEG-----RATLSRLQASVARGDPPTNELVDGGLLIA 82

Qy 53 MGSFRINPDGSQSVVEVTVPNKYA 79  
|||:||||| :|||  
Db 83 AGAFLTPGLVTDALGLFIVIPTRVA 109

RESULT 11  
T1116  
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - Florometra serratissima mitochon  
C;Species: mitochondrion Flormetra serratissima  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C;Accession: T1116  
R;Scouras, A.; Smith, M.J.  
submitted to the EMBL Data Library, February 1998  
A;Description: The complete mitochondrial genome of the crinoid Flormetra serratissima.





A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: G96607  
A;Status: Preliminary  
A;Molecule type: DNA  
A;Residues: 1-335 <STO>  
A;Cross-references: UNIPROT:Q9FXB2; UNIPARC:UPI00000A96EC; GB:AE005173; NID:g9954752; PI:  
C;Genetics:  
A;Gene: F25p12.95  
A;Map position: 1

Query Match 14.3%; Score 63.5; DB 2; Length 335;  
Best Local Similarity 27.5%; Pred. No. 22;  
Matches 19; Conservative 11; Mismatches 34; Indels 5; Gaps 3;  
Qy 19 WARSQDLHCGACRALVDELEWEIAQVDPKTI--QMGSPRINPDGS--QSVVEVTVTVP 74  
Db 151 WS-HSPQYKIGYCQCCPKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYHNLLETVKIVP 209  
Qy 75 PNKVAHSGF 83  
Db 210 PTLFAEQDF 218

Search completed: May 8, 2006, 20:57:33  
Job time : 40 secs

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 8, 2006, 20:57:05 ; Search time 46 Seconds  
(without alignments)  
149.176 Million cell updates/sec

Title: US-10-716-824-2

Perfect score: 444

Sequence: 1 MKGHWLALLGALLGTAWA.....QSVVEVTVPNKAHSGF 83

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*

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3: /cgn2\_6/ptodata/1/iaa/H-COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/pCTUS-COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/RE-COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	444	100.0	84	2	US-09-663-600A-204
2	444	100.0	85	2	US-09-716-129-63
3	410.5	92.5	97	2	US-09-663-600A-110
4	369	83.1	182	2	US-09-663-600A-205
5	369	83.1	208	2	US-09-949-016-8023
6	209.5	47.2	86	2	US-09-663-600A-111
7	109.5	24.7	419	2	US-09-893-737-106
8	96	21.6	197	2	US-09-270-767-44025
9	73	16.4	173	2	US-09-902-540-14840
10	69	15.5	803	2	US-09-252-991A-23614
11	66.5	15.0	260	2	US-09-070-526-2
12	66.5	15.0	260	2	US-09-008-271A-7
13	66.5	15.0	260	2	US-09-618-259-7
14	66.5	15.0	260	2	US-09-968-415-7
15	66.5	15.0	260	2	US-09-999-833A-395
16	66.5	15.0	260	2	US-10-020-445A-395
17	65.5	14.8	337	2	US-09-540-236-3792
18	65	14.6	4019	2	US-09-854-133-425
19	64	14.4	792	2	US-09-543-681A-6617
20	63.5	14.3	291	2	US-09-902-540-12562
21	63.5	14.3	335	2	US-09-810-506-2
22	63	14.2	149	2	US-09-270-767-47049
23	62	14.0	877	1	US-08-673-789-2
24	62	14.0	928	1	US-08-442-248-2
25	62	14.0	928	1	US-08-440-815-2
26	62	14.0	928	1	US-08-486-449-2
27	62	14.0	928	2	US-08-578-684-2

28 62 14.0 1005 1 US-08-469-537A-103 Sequence 103, App  
29 61.5 13.9 123 2 US-09-252-991A-25180 Sequence 25180, A  
30 61.5 13.9 305 2 US-09-248-796A-20913 Sequence 20913, A  
31 61.5 13.9 354 2 US-09-270-767-44204 Sequence 44204, A  
32 61 13.7 106 2 US-09-107-532A-6515 Sequence 6515, Ap  
33 61 13.7 376 2 US-09-464-535-42 Sequence 42, Appl  
34 61 13.7 1006 2 US-09-949-016-8421 Sequence 8421, Ap  
35 61 13.7 1006 2 US-09-949-016-8530 Sequence 8530, Ap  
36 60.5 13.6 271 1 US-08-447-554-4 Sequence 4, Appl  
37 60.5 13.6 271 1 US-08-448-160-4 Sequence 5, Appl  
38 60.5 13.6 1115 2 US-09-435-376-5 Sequence 11, Appl  
39 60 13.5 267 1 US-08-793-490-11 Sequence 10758, A  
40 60 13.5 296 2 US-09-949-016-10758 Sequence 909, App  
41 60 13.5 308 2 US-09-976-594-909 Sequence 909, App  
42 60 13.5 308 2 US-09-919-039-360 Sequence 360, App  
43 60 13.5 333 2 US-09-949-016-7304 Sequence 7304, Ap  
44 59.5 13.4 119 2 US-10-101-464A-832 Sequence 832, App  
45 59.5 13.4 120 2 US-09-228-986-128 Sequence 128, App

#### ALIGNMENTS

RESULT 1  
US-09-663-600A-204  
; Sequence 204, Application US/09663600A  
; Patent No. 6573068  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS  
; FILE REFERENCE: 31.US3.CIP  
; CURRENT APPLICATION NUMBER: US/09/663,600A  
; CURRENT FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: 09/191,997  
; PRIOR FILING DATE: 1998-11-13  
; PRIOR APPLICATION NUMBER: 60/066,677  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/069,957  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/074,121  
; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: 60/081,563  
; PRIOR FILING DATE: 1998-04-13  
; PRIOR APPLICATION NUMBER: 60/096,116  
; PRIOR FILING DATE: 1998-08-10  
; PRIOR APPLICATION NUMBER: 60/099,273  
; PRIOR FILING DATE: 1998-09-04  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: Patent.pm  
; SEQ ID NO 204  
; LENGTH: 84  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -20...-1  
US-09-663-600A-204

Query Match 100.0%; Score 444; DB 2; Length 84;  
Best Local Similarity 100.0%; Pred. No. 2e-49;  
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWIAQVDPKKTQMGSRINP 60  
Db 1 MKGHWLALLGALLGTAWARRSODLHCGACRALVDELEWIAQVDPKKTQMGSRINP 60  
Oy 61 DGSQSVVEVTVPNKAHSGF 83  
Db 61 DGSQSVVEVTVPNKAHSGF 83

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; SEQ ID NO 110
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -20..-1
; NAME/KEY: UNSURE
; LOCATION: 53
; OTHER INFORMATION: Xaa = any one of the twenty amino acids
US-09-663-600A-110

Query Match 92.5%; Score 410.5; DB 2; Length 97;
Best Local Similarity 94.0%; Pred. No. 4.8e-45;
Matches 79; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 MKGWGWLALLGALLGTAWARRSQDLHCGACRALVDELEWIAQVDPKKTQMGSFRINP 60
Db 1 MKGWGWLALLGALLGTAWARRSRDLHCGACRALVDELEWIAQVDPKKTQMGSFRINP 60
QY 61 DGSQSVVEVTVTVPKVAHSGF 83
Db 61 DGSQSVVEVTVTXSPKTKVAHSGF 84

RESULT 4
US-09-663-600A-205
; Sequence 205, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 205
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -20..-1
US-09-663-600A-205

Query Match 83.1%; Score 369; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 2.4e-39;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKGWGWLALLGALLGTAWARRSQDLHCGACRALVDELEWIAQVDPKKTQMGSFRINP 60
Db 1 MKGWGWLALLGALLGTAWARRSRDLHCGACRALVDELEWIAQVDPKKTQMGSFRINP 60
QY 61 DGSQSVVEVTVPKVAHSGF 69
Db 61 DGSQSVVEVTVPKVAHSGF 69

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RESULT 5
US-09-949-016-8023
; Sequence 8023, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8023
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8023

Query Match      83.1%; Score 369; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 2.9e-39;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKGWMGALLLGGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSRINP 60
DB 27 MKGWMGALLLGGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSRINP 86

QY 61 DGSQSVVEV 69
DB 87 DGSQSVVEV 95

RESULT 6
US-09-663-600A-111
; Sequence 111, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR FILING DATE: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR FILING DATE: 1997-11-13
; PRIOR FILING DATE: 1997-12-17
; PRIOR FILING DATE: 1998-02-09
; PRIOR FILING DATE: 1998-04-13
; PRIOR FILING DATE: 1998-08-10
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 111
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

Query Match      83.1%; Score 369; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 2.9e-39;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKGWMGALLLGGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSRINP 60
DB 27 MKGWMGALLLGGALLGTAWARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSRINP 86

QY 61 DGSQSVVEV 69
DB 87 DGSQSVVEV 95

RESULT 7
US-09-893-737-106
; Sequence 106, Application US/09893737
; Patent No. 6822082
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Presnell, Scott R.
; TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
; FILE REFERENCE: 00-41
; CURRENT APPLICATION NUMBER: US/09/893,737
; CURRENT FILING DATE: 2001-06-28
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 106
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-737-106

Query Match      24.7%; Score 109.5; DB 2; Length 419;
Best Local Similarity 62.9%; Pred. No. 1.7e-05;
Matches 22; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

QY 30 ACRALVDELEWEIAQVDPKKTQMGSRINPDGSG 64
DB 216 ACRALVDELEWEIAQVDPKKTQMGSRINPDGSG 249

RESULT 8
US-09-270-767-44025
; Sequence 44025, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44025
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-44025

Query Match      21.6%; Score 96; DB 2; Length 197;
Best Local Similarity 37.9%; Pred. No. 0.00034;
Matches 22; Conservative 13; Mismatches 21; Indels 2; Gaps 1;

QY 8 ALLGALLGTA--WARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSRINPDGSG 63
DB 13 ALLGALLGTA--WARRSQDLHCGACRALVDELEWEIAQVDPKKTQMGSRINPDGSG 90
```



CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/008,271A  
FILING DATE: 16-Jan-1998  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Mohan-Peterson, Sheela  
REGISTRATION NUMBER: 41,201  
REFERENCE/DOCKET NUMBER: PF-0458 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 260 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: COLNNOT27  
CLONE: 1798496  
SEQUENCE DESCRIPTION: SEQ ID NO: 7 :

US-09-008-271A-7  
Query Match 15.0%; Score 66.5; DB 2; Length 260;  
Best Local Similarity 26.0%; Pred. No. 3;  
Matches 26; Conservative 10; Mismatches 27; Indels 37; Gaps 6;  
Qy 6 WLALLGALLGTAWARRS-----ODLHCGACRALYDEL 38  
Db 12 WMFL-----LLGAWAGHSRAQEDKVLGHCQPHSQPWAALSOGQQLLCG--VLVGG- 65  
Qy 39 EWEIAQV---DPKKTIONGFSRI-NPDGQSQSVVEVTVP 74  
Db 66 NWLTAACHKPKYTVRLGDHSLQNKDGPQEIPVQSIP 105

RESULT 13  
US-09-618-259-7  
Sequence 7, Application US/09618259  
Patent No. 6642013  
GENERAL INFORMATION:  
APPLICANT: O'Brien, Timothy J.  
TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease  
FILE REFERENCE: D6020CIP2  
CURRENT APPLICATION NUMBER: US/09/618,259  
CURRENT FILING DATE: 2000-07-18  
PRIOR APPLICATION NUMBER: US 09/127,444  
PRIOR FILING DATE: 1998-08-21  
NUMBER OF SEQ ID NOS: 72  
SEQ ID NO 7  
LENGTH: 260  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Amino acid sequence of TADG-14 protein  
US-09-618-259-7  
Query Match 15.0%; Score 66.5; DB 2; Length 260;

Best Local Similarity 26.0%; Pred. No. 3;  
Matches 26; Conservative 10; Mismatches 27; Indels 37; Gaps 6;  
Qy 6 WLALLGALLGTAWARRS-----ODLHCGACRALYDEL 38  
Db 12 WMFL-----LLGAWAGHSRAQEDKVLGHCQPHSQPWAALSOGQQLLCG--VLVGG- 65  
Qy 39 EWEIAQV---DPKKTIONGFSRI-NPDGQSQSVVEVTVP 74  
Db 66 NWLTAACHKPKYTVRLGDHSLQNKDGPQEIPVQSIP 105

RESULT 14  
US-09-968-415-7  
Sequence 7, Application US/09968415  
Patent No. 6855811  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
Hillman, Jennifer L.  
Yue, Henry  
Guegler, Karl J.  
Corley, Neil C.  
Tang, Tom Y.  
Shah, Purvi  
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/968,415  
FILING DATE: 26-Sep-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/659,151  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Mohan-Peterson, Sheela  
REGISTRATION NUMBER: 41,201  
REFERENCE/DOCKET NUMBER: PF-0458 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 260 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: COLNNOT27  
CLONE: 1798496  
SEQUENCE DESCRIPTION: SEQ ID NO: 7 :

US-09-968-415-7  
Query Match 15.0%; Score 66.5; DB 2; Length 260;  
Best Local Similarity 26.0%; Pred. No. 3;  
Matches 26; Conservative 10; Mismatches 27; Indels 37; Gaps 6;  
Qy 6 WLALLGALLGTAWARRS-----ODLHCGACRALYDEL 38  
Db 12 WMFL-----LLGAWAGHSRAQEDKVLGHCQPHSQPWAALSOGQQLLCG--VLVGG- 65  
Qy 39 EWEIAQV---DPKKTIONGFSRI-NPDGQSQSVVEVTVP 74

Db 66 NWVLTAHCKPKYTVRLGDHSLQNDGPBQEIFVQVIP 105

US-09-999-833A-395  
; Sequence 395, Application US/09999833A  
; Patent No. 6916648  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630PIC55  
; CURRENT APPLICATION NUMBER: US/09/999,833A  
; CURRENT FILING DATE: 2001-10-24  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
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; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
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; PRIOR APPLICATION NUMBER: 60/077450  
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; PRIOR FILING DATE: 1998-03-13  
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;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 15.0%; Score 66.5; DB 2; Length 260;  
Best Local Similarity 26.0%; Pred. No. 3;  
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Db 12 WMFLL---LLOGAWAGHSRAQEDKVLGHECOPHSQPWQAALFOGQQLCGG--VLVGG- 65  
Qy 39 EWEIAQV---DPKKTIONGSFRI-NPDGSGSQSVVEVTVP 74  
Db 66 NWVLTAHCKKPKYIVRLGDHSLQNKDGPBEIPVVSIP 105

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